

OM protein - protein search, using sw model
Run on: December 30, 2006, 16:50:12 ; Search time 199 Seconds
(without alignments)
537.631 Million cell updates/sec

Title: US-10-063-519-14
Perfect score: 1195
Sequence: 1 MNHLPEDMENALTGSSSHA.....EAGSEAEKQDSEKPLLEL 234
Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5
2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%

Database :
Listing first 1500 summaries

A_Geneseq8:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description

RESULT 1
ID AAU29056 standard; protein; 234 AA.
DE Human PRO polypeptide sequence #33.
PN WO200168848-A2.
PD 20-SEP-2001.

Query Match 100.0%; Score 1195; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 2
ID AM39929 standard; protein; 234 AA.
DE Human polypeptide SEQ ID NO 3074.
PN WO200153312-A1.
PD 26-JUL-2001.

Query Match 100.0%; Score 1195; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 3
ID AAB87532 standard; protein; 234 AA.
DE Human PRO1864.
PN WO200116318-A2.
PD 08-MAR-2001.

Query Match 100.0%; Score 1195; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 4
ID ARG95857 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US2002119130-A1.
PD 29-AUG-2002.

Query Match 100.0%; Score 1195; DB 5; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 5
ID ABB84847 standard; protein; 234 AA.
DE Human PRO1864 protein sequence SEQ ID NO:62.
PN WO200200690-A2.
PD 03-JAN-2002.

Query Match 100.0%; Score 1195; DB 5; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 6
ID ABB95453 standard; protein; 234 AA.
DE Human angiogenesis related protein PRO1864 SEQ ID NO: 62.

PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

Query Match 100.0%; Score 1195; DB 5; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 7
ID ABUS8432 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027272-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 8
ID ABUS7980 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032127-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 9
ID ABUS4295 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032112-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 10
ID ABR66169 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027278-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 11
ID ABR65559 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036159-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 12
ID ABUS9499 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040070-A1.
PD 27-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 13
ID ABUS2738 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032113-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 14
ID ABUS9859 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036147-A1.

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PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 15
ID ABR68108 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 16
ID ABU96161 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 17
ID ABU92592 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 18
ID ABO08669 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 19
ID ABO02721 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 20
ID ABR74875 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 21
ID ABR94637 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 22
ID ABU85610 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 23
ID ABU98770 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 24
ID ABU97985 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 25
ID ABU91691 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 26
ID ABU89384 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 27
ID ABU86225 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 28
ID ABU67438 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 29
ID ABU80466 standard; protein; 234 AA.
DE Human PRO protein #33.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 30
ID ABU90882 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 31
ID ABO33941 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 32
ID ABR99384 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 33
ID ABR98774 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 34
ID ABO16297 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027267-A1.
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PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 35
ID ABR92197 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 36
ID ABO18838 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 37
ID ABR78259 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 38
ID ABR39937 standard; protein; 234 AA.
DE Human prostate selective polypeptide Pr340.
PN WO2003014298-A2.
PD 20-FEB-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 39
ID ABR71958 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 40
ID ABU84995 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 41
ID ABO00134 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 42
ID ABO11466 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 43
ID ABO02111 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 44
ID ABU86885 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036133-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 45
ID ABU83380 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 46
ID ABO06181 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 47
ID ABR59217 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 48
ID ABO09279 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 49
ID ABO19143 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 50
ID ABO11161 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 51
ID ABR66779 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 52
ID ABO15992 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 53
ID ABO13698 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 54
ID ABU71512 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 55
ID ABO07754 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 56
ID ABO07449 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 57
ID ABO03636 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 58
ID ABR67084 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 59
ID ABO15687 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 60
ID ABUS5968 standard; protein; 234 AA.
DE Human secreted/transmembrane protein, PRO1864.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 61
ID ABU72293 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 62
ID ABU65296 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 63
ID ABUS5241 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 64
ID ABU71144 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 65
ID ABO07754 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 66
ID ABR6995 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 67
ID ABR69328 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 68
ID ABO01469 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 69
ID ABU81271 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 70
ID ABR60068 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 71
ID ABR58287 standard; protein; 234 AA.
DE BCU0092 protein #SEQ ID 20.
PN WO2003029421-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 72
ID ABUS0966 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 73
ID ABR67803 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 74
ID ABR65191 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027268-A1.
PD 06-FEB-2003.
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Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 75
ID ABR68413 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 76
ID ABR71825 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 77
ID ABU85305 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 78
ID ABU88995 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 79
ID ABU83075 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 80
ID ABU94931 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 81
ID ABU90479 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 82
ID ABU83990 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 83
ID ABU93641 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 84
ID ABR64886 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 85
ID ABO27287 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO1864.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 86
ID ABR68718 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 87
ID ABO6534 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 88
ID ABR99079 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 89
ID ARU56963 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 90
ID ABU85915 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 91
ID ABU82202 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 92
ID ABU87213 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 93
ID ABU83685 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 94
ID ABO8059 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 95
ID ABR68413 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;

ID ABU92482 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 96
ID ABU81770 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 97
ID ABU65934 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 98
ID ABU81152 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 99
ID ABR59763 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 100
ID ABU93951 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 101
ID ABU99804 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 102
ID ABR66474 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 103
ID ABR90892 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 104
ID ABO53267 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 105
ID ABU79506 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 106
ID ABU79201 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 107
ID ABU86530 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 108
ID ABU86835 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 109
ID ABU94624 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 110
ID ABO04551 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 111
ID ABR70300 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 112
ID ABU98465 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 113
ID ABR65864 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 114
ID ABR64581 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027282-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 115
ID ABU79506 standard; protein; 234 AA.

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DE Human PRO polypeptide #33.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 116
ID ABU92897 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 117
ID ABU95856 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 118
ID ABU91076 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 119
ID ABU90169 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 120
ID ABO09584 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 121
ID ABO10856 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 122
ID ABR70910 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 123
ID ABU98269 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 124
ID ABU87518 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 125
ID ABU91386 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 126
ID ABU89274 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 127
ID ABU84600 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 128
ID ABR69690 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 129
ID ASU80067 standard; protein; 234 AA.
DE Human PRO protein #33.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 130
ID ABU82481 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 131
ID ABU93336 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 132
ID ABO09889 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 133
ID ABO08974 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 134
ID ABU96445 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 135
ID ABU10542 standard; protein; 234 AA.
DE Human secreted/transmembrane protein #33.
PN US2002127584-A1.
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PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 136
ID ABR72115 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 137
ID ABR95551 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 138
ID ABR96760 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 139
ID ABR70605 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 140
ID ABO04956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 141
ID ABO08364 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 142
ID ABO05571 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 143
ID ABR73960 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 144
ID ABR95552 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 145
ID ABR08049 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 146
ID ABR81154 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 147
ID ABO00850 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 148
ID ABR88452 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 149
ID ABR77273 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 150
ID ABO28757 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 151
ID ABO31502 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 152
ID ABO7919 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 153
ID ABO40399 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 154
ID ABO35824 standard; protein; 234 AA.
DE Human PRO polypeptide #33.

PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 155
ID ABO43963 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 156
ID ADA77818 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 157
ID ABR97749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 158
ID ABO3026 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 159
ID ABR90282 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 160
ID ABM17196 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 161
ID ABR94942 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 162
ID ABR95247 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 163
ID ADB17071 standard; protein; 234 AA.
DE Human transmembrane PRO polypeptide (SeqID 14).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 164
ID ABO21485 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 165
ID ABR97749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 166
ID ABR87537 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 167
ID ABM77578 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 168
ID ABR27808 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 169
ID ABM06089 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 170
ID ABM03595 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003088722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 171
ID ABM35046 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 172
ID ABM26283 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 173
ID ABO48065 standard; protein; 234 AA.

DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003049749-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 174
 ID ABR92807 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003064462-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 175
 ID ABO24568 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003065159-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 176
 ID ABM1579 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003064447-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 177
 ID ABM02680 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003073184-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 178
 ID ABM15976 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003064463-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 179
 ID ABO27537 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003064451-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 180
 ID ABM29028 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003068721-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 181
 ID ABM07004 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003068699-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 182
 ID ABM21098 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN US2003068707-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 183
 ID ABM09444 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003073175-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 184
 ID ABO41314 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003068695-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 185
 ID ABO36129 standard; protein; 234 AA.
 DE Human PRO polypeptide #33.
 PN US2003068703-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 186
 ID ABO43658 standard; protein; 234 AA.
 DE Human PRO polypeptide #33.
 PN US2003068732-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 187
 ID ABM76358 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003082717-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 188
 ID ABM76054 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003104548-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 189
 ID ABM25673 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003104542-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 190
 ID ABM25978 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003104543-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 191
 ID ABO33331 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003036127-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 6; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 192
ID ABO02416 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 193
ID ABO44245 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 194
ID ABR90587 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 195
ID ABR73655 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 196
ID ABO16907 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 197
ID ABR94332 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 198
ID ABR75839 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 199
ID ABR71215 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 200
ID ABR93112 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 201
ID ABR93417 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054478-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 202
ID ABR87842 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 203
ID ABO27842 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 204
ID ABO29977 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 205
ID ABO33186 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 206
ID ABO4874 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 207
ID ABO80834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 208
ID ABO36434 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 209
ID ABO35519 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 210
ID ABO39484 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 211
ID ABM10359 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 212
ID ABM11884 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 213
ID ABO52030 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 214
ID ABO52335 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 215
ID ADA19876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 216
ID ABO23653 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 217
ID ADB17259 standard; protein; 234 AA.
DE Human transmembrane PRO polypeptide (SeqID 14).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 218
ID ABR97139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 219
ID ABR86927 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 220
ID ABM10969 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 221
ID ABM28113 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 222
ID ABO32112 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 223
ID ABM15239 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 224
ID ABM06394 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 225
ID ABM04205 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 226
ID ABM22318 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 227
ID ABM07614 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 228
ID ABO40704 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 229
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ID ABM35351 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 230
ID ABM31114 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 231
ID ABO52640 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 232
ID ABO50200 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 233
ID ABU99194 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 234
ID ABO04246 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 235
ID ABO05876 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 236
ID ABM18416 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 237
ID ABR97444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 238
ID ABR80544 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 239
ID ABM01155 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 240
ID ABR88757 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 241
ID ABM13409 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 242
ID ABM20793 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 243
ID ABO41924 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 244
ID ABO42534 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 245
ID ABM10054 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 246
ID ABO38569 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 247
ID ABM32809 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 248
ID ABM22623 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 249
ID ABM74834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 250
ID ADA79610 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 251
ID ABR96224 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 252
ID ABM02375 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 253
ID ABR86317 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 254
ID ABR86622 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 255
ID ABM16586 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 256
ID ABR29638 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 257
ID ABO29062 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 258
ID ABM23843 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 259
ID ABM23233 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 260
ID ABM22013 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 261
ID ABO37654 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 262
ID ABM28418 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 263
ID ABM28723 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 264
ID ABM66367 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 265
ID ABM75749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 266
ID ABM34029 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 267
ID ABM34334 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
ID ABO20265 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
ID ABO21180 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
ID ABO22095 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
ID ADA20048 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003052222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
ID ABO34173 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
ID ABR96529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
ID ABR85707 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
ID ABR99689 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
ID ABM00545 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 277
ID ABM00240 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 278
ID ABO29672 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 279
ID ABM23538 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 280
ID ABM29333 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 281
ID ABO38264 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 282
ID ASO45564 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 283
ID ABM20488 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 284
ID ADA81337 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 285
ID ABO16602 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 286
ID ABO18228 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 287
ID ABO22655 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 288
ID ABO22960 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 289
ID ABR92502 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 290
ID ABR81459 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 291
ID ABR77883 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 292
ID ABR89672 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 293
ID ABR26588 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 294
ID ABR13714 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 295
ID ABO28452 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064460-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 296
ID ABO30282 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 297
ID ABO70309 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 298
ID ABO3900 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 299
ID ABO37044 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 300
ID ABO41619 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 301
ID ABO35214 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 302
ID ABR25063 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 303
ID ABO47455 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 304
ID ABO47760 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 305
ID ABO48370 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 306
ID ABO51420 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 307
ID ABO51725 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 308
ID ABO50505 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 309
ID ABR79629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 310
ID ABR79629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 311
ID ABO17923 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 312
ID ABO20875 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 313
ID ABR96834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 314
ID ABR12189 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 315
ID ABR16281 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 316
ID ABR24148 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 317
ID ABR14629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 318
ID ABR04510 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 319
ID ABR06699 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 320
ID ABR09139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 321
ID ABO39179 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 322
ID ABR75444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 323
ID ABR25368 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104541-A1.
PD 05-JUN-2003.

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Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 324
ID ABM19878 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 325
ID ABO46784 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 326
ID ABO47089 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 327
ID ADA83135 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 328
ID ABR71520 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 329
ID ABR72130 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 330
ID ABR98469 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 331
ID ABO06839 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 332
ID ABR84792 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 333
ID ABR73350 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 334
ID ABR76444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 335
ID ABR73045 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 336
ID ABM18111 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 337
ID ABO20570 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 338
ID ABO25313 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 339
ID ABO25618 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 340
ID ABR94027 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 341
ID ABR79934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 342
ID ABM11274 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 343
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ID ABO32881 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 344
ID ABO30587 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 345
ID ABO30892 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 346
ID ABO27198 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 347
ID ABO29943 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 348
ID ABO5479 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 349
ID ABO15544 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 350
ID ABO08529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 351
ID ABO42229 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 352
ID ABO37959 standard; protein; 234 AA.

DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 353
ID ABO45869 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 354
ID ABO66672 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 355
ID ABO20178 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 356
ID ABO19573 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 357
ID ABO49285 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 358
ID ABO49590 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 359
ID ADA78430 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 360
ID ABO88147 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 361
ID ADA00345 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003027992-A1.

PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 362
ID ABR26893 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 363
ID ABO03290 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 364
ID ABO39789 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 365
ID ABO49895 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 366
ID ABO50810 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 367
ID ABO5266 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 368
ID ABR74570 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 369
ID ABR77049 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 370
ID ABR17806 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 371

ID ABR95857 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 372
ID ABO21790 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 373
ID ABO19960 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 374
ID ABO24263 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 375
ID ABR86012 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 376
ID ABR10664 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 377
ID ABR76663 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 378
ID ABR89367 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 379
ID ABR12494 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 380
ID ABR05784 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068717-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 381
ID ABO34909 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 382
ID ABO2985 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 383
ID ABO18963 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 384
ID ABO19268 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 385
ID ABO46479 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 386
ID ABO48980 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 387
ID ABR69023 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 388
ID ABR89062 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 389
ID ABR72435 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 390

ID ABR74265 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 391
ID ABO18533 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 392
ID ABR80239 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 393
ID ABO1460 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 394
ID ABO2070 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 395
ID ABR87232 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 396
ID ABO12799 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 397
ID ABO30553 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 398
ID ABO24453 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 399
ID ABO29367 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.

PN US2003068697-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 400
 ID ABO31197 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003068710-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 401
 ID ABM14324 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003068686-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 402
 ID ABM09749 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003073178-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 403
 ID ABO38874 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003068774-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 404
 ID ABM34639 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003104538-A1.
 PD 05-JUN-2003.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 405
 ID ABO51115 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003049781-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 406
 ID ABO03941 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003036158-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 407
 ID ABO10411 standard; protein; 234 AA.
 DE Human PRO polypeptide #33.
 PN US2003036151-A1.
 PD 20-FEB-2003.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 408
 ID ABR77654 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003040067-A1.
 PD 27-FEB-2003.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 409
 ID ABR78864 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003054456-A1.
 PD 20-MAR-2003.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 410
 ID ABO23958 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003054482-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 411
 ID ABR93722 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003054457-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 412
 ID ABM01765 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003059883-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 413
 ID ABM78188 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003049764-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 414
 ID ABR89977 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003073177-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 415
 ID ABM27503 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003064442-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 416
 ID ABM13104 standard; protein; 234 AA.
 DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
 PN US2003064450-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 417
 ID ABO31807 standard; protein; 234 AA.
 DE Human secreted/transmembrane protein (PRO) #33.
 PN US2003068731-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 418
 ID ABM14019 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 419
ID ABM08224 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 420
ID AB040094 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 421
ID ABM74529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 422
ID ABM33724 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 423
ID ABM20183 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 424
ID AB048675 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 425
ID ABR72740 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 426
ID AB015382 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 427
ID ABR85097 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 428
ID ABO15077 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 429
ID ABO17212 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 430
ID ABM17501 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 431
ID ABR85402 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 432
ID ABM76968 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 433
ID ABO28147 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 434
ID ABM22928 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 435
ID ABM30248 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 436
ID ABM21708 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 437
ID ABM21403 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 438
ID ABM14934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 439
ID ABO41009 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 440
ID ABO36739 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 441
ID ABO37349 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 442
ID ABM75139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 443
ID ABM33419 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 444
ID ABO46174 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 445
ID ADA82501 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 446
ID ADB85587 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003049735-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 447
ID ABM31773 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 448
ID ABM31163 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 449
ID ADB85809 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 450
ID ABM32078 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 451
ID ABM32383 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 452
ID ADB68266 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 453
ID ADB68073 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 454
ID ABM31468 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 455
ID ABM30858 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 456
ID ADB90890 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 457
ID ADC06970 standard; protein; 234 AA.
DE Human secreted/transmembrane protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 458
ID ADC17149 standard; protein; 234 AA.
DE Mammalian PRO polypeptide (SeqID 14).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 459
ID ADC14847 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 460
ID ADC52342 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 461
ID ADD05539 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 462
ID ADD10351 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 463
ID ADD11311 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 464
ID ADD37104 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 465
ID ADD36018 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 466
ID ADG01019 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 467
ID ADG08572 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 468
ID ADG02534 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 469
ID ADG01241 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 470
ID ADF95416 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 471
ID ADF95193 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 472
ID ADG12231 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 473
ID ADH24046 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 474

ID ADH34072 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 475
ID ADH23905 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 476
ID ADH23876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 477
ID ADH08891 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 478
ID ADH85280 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 479
ID ADH24556 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 480
ID ADH37412 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 481
ID ADH02001 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 482
ID ADH37582 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 483
ID ADG85620 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 484
ID ADH24216 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 485
ID ADH38510 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 486
ID ADG83631 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 487
ID ADH29439 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 488
ID ADH27555 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 489
ID ADH37752 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 490
ID ADH37929 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 491
ID ADH57349 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 492
ID ADH53491 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.

PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 493
ID ADH53661 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 494
ID ADH51997 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 495
ID ADH49852 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 496
ID ADI25362 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 497
ID ADH90155 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 498
ID ADI25532 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 499
ID ADH97706 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 500
ID ADI03554 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 501
ID ADI11911 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181686-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 502
ID ADH89985 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 503
ID ADH98386 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 504
ID ADI11061 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 505
ID ADI11571 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 506
ID ADH98216 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 507
ID ADH98556 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 508
ID ADH98046 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 509
ID ADI05034 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 510
ID ADI03384 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181654-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 511
 ID ADI04779 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003181657-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 512
 ID ADH78233 standard; protein; 234 AA.
 DE Human PRO polypeptide #7.
 PN US2003181668-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 513
 ID ADI19577 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003181676-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 514
 ID ADH90325 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003181699-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 515
 ID ADI03044 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003181653-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 516
 ID ADH77893 standard; protein; 234 AA.
 DE Human PRO polypeptide #7.
 PN US2003181666-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 517
 ID ADH97876 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003181674-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 518
 ID ADI01261 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003190669-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 519
 ID ADI01956 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003181652-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 520
 ID ADI03214 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003181655-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 521
 ID ADI11401 standard; protein; 234 AA.
 DE Human PRO polypeptide #7.
 PN US2003181681-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 522
 ID ADI02303 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003181650-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 523
 ID ADI11741 standard; protein; 234 AA.
 DE Human PRO polypeptide #7.
 PN US2003181685-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 524
 ID ADI05378 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003190716-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 525
 ID ADH79450 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003191290-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 526
 ID ADI19407 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003181675-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 527
 ID ADI05208 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003181677-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1195; DB 7; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.6e-131;
 RESULT 528
 ID ADH79620 standard; protein; 234 AA.
 DE Novel human secreted and transmembrane protein PRO1864.
 PN US2003191288-A1.
 PD 09-OCT-2003.
 PA (GETH) GENENTECH INC.

RESULT 538
ID ADK65384 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003073921-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 539
ID ADH98726 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 540
ID ADH79967 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 541
ID ADL32672 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 542
ID ADM30206 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 543
ID ADU93698 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 544
ID ADC52152 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 545
ID ADB41312 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
FN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 546
ID ADE74203 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
FN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 547
ID ADE74815 standard; protein; 234 AA.

DE Human secreted/transmembrane protein (PRO) #33.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 548
ID ADF96028 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 549
ID ADG04299 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 550
ID ADG00459 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 551
ID ADH06584 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 552
ID ADH06414 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 553
ID ADG68835 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 554
ID ADH27725 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 555
ID ADH25066 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 556
ID ADH33698 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181645-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 557
ID ADG82715 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 558
ID ADH02341 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 559
ID ADH07948 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 560
ID ADG69345 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 561
ID ADH39166 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 562
ID ADH25996 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 563
ID ADG83906 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 564
ID ADG85450 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003186848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 565
ID ADH06244 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 566
ID ADH30074 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 567
ID ADH24386 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 568
ID ADH32965 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
FN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 569
ID ADG69515 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 570
ID ADH07778 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 571
ID ADG85790 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 572
ID ADH39336 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 573
ID ADH33528 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
FN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 574
ID ADH33868 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
FN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 575
ID ADH01078 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
FN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 575
ID ADH01078 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
FN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 576
ID ADG69685 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 577
ID ADH02171 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
FN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 578
ID ADG69175 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 579
ID ADG85960 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 580
ID ADH24896 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 581
ID ADH39513 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 582
ID ADH02511 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
FN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 583
ID ADG69005 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
FN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 584
ID ADH33868 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
FN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 8; Length 234;
RESULT 585
ID ADH33868 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
FN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

RESULT 584
ID ADH07608 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 585
ID ADG86130 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 586
ID ADH24726 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 587
ID ADH25774 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 588
ID ADH38340 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 589
ID ADH57179 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 590
ID ADH43495 standard; protein; 234 AA.
DE Human PRO polypeptide #31.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 591
ID ADH52167 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 592
ID ADH49533 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 593
ID ADH90495 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 594
ID ADI11231 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 595
ID ADH98896 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 596
ID ADI02126 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 597
ID ADH90665 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 598
ID ADJ54704 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 599
ID ADJ98540 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 600
ID ADJ98710 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 601
ID ADH78869 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 602
ID ADJ99103 standard; protein; 234 AA.

DE Novel human secreted and transmembrane protein PRO1864.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 603
ID ADJ99273 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 604
ID ADJ98891 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 605
ID ADH79039 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 606
ID ADK00899 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 607
ID ADK14420 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 608
ID ADK82840 standard; protein; 234 AA.
DE Human PRO polypeptide #31.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 609
ID ADJ64475 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 610
ID ADM31371 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 611
ID ADM36418 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.

PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 612
ID ADM40223 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 613
ID ADM80869 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 614
ID ADJ18173 standard; protein; 234 AA.
DE Human PRO1864 protein SEQ ID NO:94.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 615
ID ADN37831 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 616
ID ADY18016 standard; protein; 234 AA.
DE PRO polypeptide SEQ ID NO 3822.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 9; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 617
ID ADY19397 standard; protein; 234 AA.
DE PRO polypeptide SEQ ID NO 5203.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 9; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 618
ID ADY77709 standard; protein; 234 AA.
DE Neoplastic disease detection protein PRO1864.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO)/ EATON D L.
PA (FILV)/ FILVAROFF E.
PA (GERR)/ GERRITSEN M E.
PA (GODD)/ GODDARD A.
PA (GODO)/ GODOWSKI P J.
PA (GRIM)/ GRIMALDI J C.
PA (GURN)/ GURNEY A L.
PA (WATA)/ WATANABE C K.
PA (WOOD)/ WOOD W I.
Query Match 100.0%; Score 1195; DB 9; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 619
ID AEA08359 standard; protein; 234 AA.
DE Steriodogenic acute regulatory protein related (MLN64).
PN WO2005047536-A2.

PD 26-MAY-2005.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match 100.0%; Score 1195; DB 9; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 620
ID AED50061 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2005163766-A1.
PD 28-JUL-2005.
Query Match 100.0%; Score 1195; DB 9; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 621
ID AEF12540 standard; protein; 234 AA.
DE Human PRO1864 protein SEQ ID NO:14.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 622
ID AEF74229 standard; protein; 234 AA.
DE Human PRO1864 protein SEQ ID NO:14.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 100.0%; Score 1195; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 623
ID AAM41716 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 6647.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1195; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.7e-131;
RESULT 624
ID AAM41715 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 6646.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1195; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.7e-131;
RESULT 625
ID ABP75508 standard; protein; 238 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 692.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 100.0%; Score 1195; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.7e-131;
RESULT 626
ID ABR58404 standard; protein; 234 AA.
DE Human NOV19b.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 99.4%; Score 1188; DB 6; Length 234;
Best Local Similarity 99.6%; Pred. No. 1.1e-130;
RESULT 627
ID AAM39930 standard; protein; 216 AA.
DE Human polypeptide SEQ ID NO 3075.
PN WO200153312-A1.
PD 26-JUL-2001.

PA (HYSE-) HYSEQ INC.
Query Match 91.8%; Score 1097; DB 4; Length 216;
Best Local Similarity 92.3%; Pred. No. 4.9e-120;
RESULT 628
ID ABB90287 standard; protein; 201 AA.
DE Human polypeptide SEQ ID NO 2663.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 85.7%; Score 1024; DB 5; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.7e-111;
RESULT 629
ID ABR58403 standard; protein; 198 AA.
DE Human NOV19a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 82.4%; Score 985; DB 6; Length 198;
Best Local Similarity 84.6%; Pred. No. 6.5e-107;
RESULT 630
ID AAU30250 standard; protein; 283 AA.
DE Novel human secreted protein #741.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 65.0%; Score 777; DB 4; Length 283;
Best Local Similarity 72.5%; Pred. No. 3.2e-82;
RESULT 631
ID ADB64413 standard; protein; 176 AA.
DE Human protein encoded by clone FEBRA20007820.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 56.0%; Score 669.5; DB 7; Length 176;
Best Local Similarity 87.5%; Pred. No. 7.2e-70;
RESULT 632
ID ADK36828 standard; protein; 146 AA.
DE Novel human polypeptide SeqID8910.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 55.6%; Score 665; DB 5; Length 146;
Best Local Similarity 91.0%; Pred. No. 1.9e-69;
RESULT 633
ID ADZ88813 standard; protein; 383 AA.
DE Breast specific protein SEQ ID NO 180.
PN WO2005044075-A2.
PD 19-MAY-2005.
PA (DIAD-) DIADEXUS INC.
Query Match 55.6%; Score 664; DB 9; Length 383;
Best Local Similarity 56.2%; Pred. No. 9.4e-69;
RESULT 634
ID AAW25768 standard; protein; 445 AA.
DE Human MLN 64.
PN WO9706256-A2.
PD 20-FEB-1997.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
PA (CNRS) CENT NAT RECH SCI.
PA (UYPA-) UNIV PASTEUR LOUIS.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 55.6%; Score 664; DB 2; Length 445;
Best Local Similarity 56.2%; Pred. No. 1.2e-68;
RESULT 635
ID ABR47530 standard; protein; 445 AA.
DE Breast cancer associated protein sequence SEQ ID NO:296.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 55.6%; Score 664; DB 6; Length 445;
Best Local Similarity 56.2%; Pred. No. 1.2e-68;
RESULT 636
ID ADH13184 standard; protein; 445 AA.

DE Human malignant neoplasia-related protein SeqID33.
PN EP1365034-A2.
PD 26-NOV-2003.
PA (FARB) BAYER AG.
Query Match 55.6%; Score 664; DB 8; Length 445;
Best Local Similarity 56.2%; Pred. No. 1.2e-68;
RESULT 637
ID AEAL5071 standard; protein; 445 AA.
DE Human polypeptide #7.
PN WO2005047534-A2.
PD 26-MAY-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 55.6%; Score 664; DB 9; Length 445;
Best Local Similarity 56.2%; Pred. No. 1.2e-68;
RESULT 638
ID AD28812 standard; protein; 497 AA.
DE Breast specific protein SEQ ID NO 179.
PN WO2005044075-A2.
PD 19-MAY-2005.
PA (DIAD-) DIADEXUS INC.
Query Match 55.6%; Score 664; DB 9; Length 497;
Best Local Similarity 56.2%; Pred. No. 1.4e-68;
RESULT 639
ID ABG05498 standard; protein; 534 AA.
DE Novel human diagnostic protein #5489.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 52.3%; Score 625; DB 4; Length 534;
Best Local Similarity 48.9%; Pred. No. 5.8e-64;
RESULT 640
ID ABR69622 standard; protein; 412 AA.
DE Human CGDD-22 protein.
PN WO2003027263-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 48.4%; Score 578; DB 6; Length 412;
Best Local Similarity 58.3%; Pred. No. 1.4e-58;
RESULT 641
ID ABP75900 standard; protein; 111 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1084.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 33.9%; Score 405.5; DB 6; Length 111;
Best Local Similarity 73.7%; Pred. No. 4.4e-39;
RESULT 642
ID ABB59968 standard; protein; 580 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6696.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 28.7%; Score 343; DB 4; Length 580;
Best Local Similarity 37.8%; Pred. No. 9.7e-31;
RESULT 643
ID AAM90384 standard; protein; 70 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:17977.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.9%; Score 322; DB 4; Length 70;
Best Local Similarity 98.4%; Pred. No. 1.5e-29;
RESULT 644
ID AAB96837 standard; protein; 424 AA.
DE Putative P. abyssi nucleoside-diphosphate-sugar pyrophosphorylase #6.
PN FR292651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 7.8%; Score 93.5; DB 4; Length 424;
Best Local Similarity 21.9%; Pred. No. 0.14;
RESULT 645
ID AAU03699 standard; protein; 373 AA.

DE Group B Streptococcus antigenic protein, ID-176.
PN WO200132882-A2.
PD 10-MAY-2001.
PA (MICR-) MICROBIAL TECHNIQS LTD.
Query Match 7.8%; Score 91; DB 4; Length 373;
Best Local Similarity 25.7%; Pred. No. 0.23;
RESULT 646
ID ADV89705 standard; protein; 605 AA.
DE Streptococcus agalactiae protein sequence, SEQ ID 2099.
PN FR2824074-A1.
PD 31-OCT-2002.
PA (INSP) INST PASTEUR.
Query Match 7.6%; Score 91; DB 8; Length 605;
Best Local Similarity 25.7%; Pred. No. 0.46;
RESULT 647
ID ADV80958 standard; protein; 605 AA.
DE Streptococcus agalactiae protein, SEQ ID 2099.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 7.8%; Score 91; DB 8; Length 605;
Best Local Similarity 25.7%; Pred. No. 0.46;
RESULT 648
ID ABP30317 standard; protein; 651 AA.
DE Streptococcus polypeptide SEQ ID NO 9810.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.6%; Score 91; DB 5; Length 651;
Best Local Similarity 25.7%; Pred. No. 0.5;
RESULT 649
ID ADV83104 standard; protein; 651 AA.
DE Streptococcus agalactiae protein, SEQ ID 4245.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 7.8%; Score 91; DB 8; Length 651;
Best Local Similarity 25.7%; Pred. No. 0.5;
RESULT 650
ID ABP29732 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 8640.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.6%; Score 91; DB 5; Length 654;
Best Local Similarity 25.7%; Pred. No. 0.51;
RESULT 651
ID ABP26469 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 2114.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.8%; Score 91; DB 5; Length 654;
Best Local Similarity 25.7%; Pred. No. 0.51;
RESULT 652
ID AAG61678 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80037.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 87.5; DB 3; Length 155;
Best Local Similarity 21.4%; Pred. No. 0.18;
RESULT 653
ID AAG59838 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77441.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 87.5; DB 3; Length 155;

Best Local Similarity 21.4%; Pred. No. 0.18;
RESULT 654
ID AAB58945 standard; protein; 516 AA.
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 653.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.3%; Score 87.5; DB 3; Length 516;
Best Local Similarity 25.3%; Pred. No. 0.94;
RESULT 655
ID ADQ39266 standard; protein; 421 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 929.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.3%; Score 87; DB 8; Length 421;
Best Local Similarity 23.7%; Pred. No. 0.81;
RESULT 656
ID ADQ39263 standard; protein; 223 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 926.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 223;
Best Local Similarity 25.5%; Pred. No. 0.51;
RESULT 657
ID ADQ39258 standard; protein; 285 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 921.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 285;
Best Local Similarity 25.5%; Pred. No. 0.71;
RESULT 658
ID ADQ39262 standard; protein; 315 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 925.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 315;
Best Local Similarity 25.5%; Pred. No. 0.82;
RESULT 659
ID ADQ39260 standard; protein; 323 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 923.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 323;
Best Local Similarity 25.5%; Pred. No. 0.85;
RESULT 660
ID ADQ39261 standard; protein; 328 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 924.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 328;
Best Local Similarity 25.5%; Pred. No. 0.86;
RESULT 661
ID ADQ39265 standard; protein; 338 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 928.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 338;
Best Local Similarity 25.5%; Pred. No. 0.9;
RESULT 662
ID ADQ39267 standard; protein; 339 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 930.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 339;
Best Local Similarity 25.5%; Pred. No. 0.9;

RESULT 663
ID ADE28099 standard; protein; 340 AA.
DE Human NTRAN protein - SEQ ID 4.
PN WO2003051902-A1.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.2%; Score 85.5; DB 7; Length 340;
Best Local Similarity 25.5%; Pred. No. 0.91;
RESULT 664
ID ADQ39269 standard; protein; 384 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 932.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 384;
Best Local Similarity 25.5%; Pred. No. 1.1;
RESULT 665
ID ADQ39264 standard; protein; 390 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 927.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 390;
Best Local Similarity 25.5%; Pred. No. 1.1;
RESULT 666
ID ABU26680 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #12207.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 85.5; DB 6; Length 396;
Best Local Similarity 21.0%; Pred. No. 1.1;
RESULT 667
ID AAW13575 standard; protein; 438 AA.
DE Batten disease polypeptide CLN3.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 668
ID AAW13589 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L204.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 24.8%; Pred. No. 1.3;
RESULT 669
ID AAW13582 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L46.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 670
ID AAW13577 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L39.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 671
ID ADQ96392 standard; protein; 438 AA.
DE T cell activation associated protein #285.
PN WO2004058805-A2.
PD 15-JUL-2004.

PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 672
ID ADQ39268 standard; protein; 438 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 931.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 673
ID ADA05822 standard; protein; 440 AA.
DE Human NOV434 protein SEQ ID NO:182.
PN WO2003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.2%; Score 85.5; DB 6; Length 440;
Best Local Similarity 25.2%; Pred. No. 1.3;
RESULT 674
ID ADM63244 standard; protein; 440 AA.
DE Human NOV434 variant.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (ELLE/) ELLERMAN K.
PA (EDIN/) EDINGER S R.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match 7.2%; Score 85.5; DB 8; Length 440;
Best Local Similarity 25.2%; Pred. No. 1.3;
RESULT 675
ID ADM62985 standard; protein; 440 AA.
DE Human NOV434.
PN US2004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 676
ID AED74247 standard; protein; 449 AA.
DE Human placental protein SEQ ID NO:1075.
PN US2005255114-A1.
PD 17-NOV-2005.
PA (NUVE-) NUVELO INC.
Query Match 7.2%; Score 85.5; DB 9; Length 449;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 677
ID AAW13593 standard; protein; 467 AA.
DE Batten disease CLN3 mutant protein in family L61.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEHO/) GEN HOSPITAL CORP.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 7.2%; Score 85.5; DB 2; Length 467;
Best Local Similarity 25.5%; Pred. No. 1.4;
RESULT 678
ID ABB89640 standard; protein; 473 AA.
DE Human polypeptide SEQ ID NO 2016.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.2%; Score 85.5; DB 5; Length 473;
Best Local Similarity 25.2%; Pred. No. 1.4;
RESULT 679
ID ADQ18055 standard; protein; 473 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 872.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.2%; Score 85.5; DB 8; Length 473;
Best Local Similarity 25.2%; Pred. No. 1.4;
RESULT 680
ID ADU06406 standard; protein; 473 AA.
DE Novel bronchial cancer-associated human protein SeqID630.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 7.2%; Score 85.5; DB 8; Length 473;
Best Local Similarity 25.2%; Pred. No. 1.4;
RESULT 681
ID ADY20253 standard; protein; 473 AA.

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DE PRO polypeptide SEQ ID NO 6059.
PN WO2005016962-A2.
PA (GETH ) GENENTECH INC.
  Query Match 7.2%; Score 85.5; DB 9; Length 473;
  Best Local Similarity 25.2%; Pred. No. 1.4;
RESULT 682
ID ABU40544 standard; protein; 500 AA.
DE Protein encoded by Prokaryotic essential gene #26071.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match 7.2%; Score 85.5; DB 6; Length 500;
  Best Local Similarity 26.0%; Pred. No. 1.6;
RESULT 683
ID ADY09432 standard; protein; 527 AA.
DE Plant full length insert polypeptide seqid 65247.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
  Query Match 7.1%; Score 85; DB 8; Length 527;
  Best Local Similarity 17.6%; Pred. No. 1.9;
RESULT 684
ID ABU33210 standard; protein; 430 AA.
DE Protein encoded by Prokaryotic essential gene #18737.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match 7.1%; Score 84.5; DB 6; Length 430;
  Best Local Similarity 25.5%; Pred. No. 1.6;
RESULT 685
ID AAW13588 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L10.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEOH ) GEN HOSPITAL CORP.
PA (UYLE-) RIJXSUNIV LEIDEN.
  Query Match 7.1%; Score 84.5; DB 2; Length 438;
  Best Local Similarity 24.8%; Pred. No. 1.7;
RESULT 686
ID AAG16921 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17749.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match 7.0%; Score 83.5; DB 3; Length 322;
  Best Local Similarity 33.7%; Pred. No. 1.4;
RESULT 687
ID ABG21285 standard; protein; 472 AA.
DE Novel human diagnostic protein #21276.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 7.0%; Score 83.5; DB 4; Length 472;
  Best Local Similarity 20.1%; Pred. No. 2.5;
RESULT 688
ID ABU35608 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #21135.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match 6.9%; Score 82.5; DB 6; Length 239;
  Best Local Similarity 21.7%; Pred. No. 1.3;
RESULT 689
ID ADU25550 standard; protein; 389 AA.
DE L. acidophilus cell surface protein homologue #63.
PN WO2004096992-A2.
PD 11-NOV-2004.
PA (UYNC-) UNIV NORTH CAROLINA STATE.
  Query Match 6.9%; Score 82.5; DB 8; Length 389;
  Best Local Similarity 24.7%; Pred. No. 2.5;
RESULT 690
ID AAW13590 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L216.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEOH ) GEN HOSPITAL CORP.
PA (UYLE-) RIJXSUNIV LEIDEN.
  Query Match 6.9%; Score 82.5; DB 2; Length 438;
  Best Local Similarity 24.8%; Pred. No. 2.9;
RESULT 691
ID ADB85263 standard; protein; 589 AA.
DE Mouse RNAL homologue SEQ ID NO:144.
PN EP1284297-A2.
PD 19-FEB-2003.
PA (WARN ) WARNER LAMBERT CO.
  Query Match 6.9%; Score 82; DB 7; Length 589;
  Best Local Similarity 19.5%; Pred. No. 5;
RESULT 692
ID ADX74800 standard; protein; 264 AA.
DE Plant full length insert polypeptide seqid 44166.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
  Query Match 6.8%; Score 81.5; DB 8; Length 264;
  Best Local Similarity 33.3%; Pred. No. 1.9;
RESULT 693
ID AAW13586 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L285.
PN WO9708308-A1.
PD 06-MAR-1997.
PA (GEOH ) GEN HOSPITAL CORP.
PA (UYLE-) RIJXSUNIV LEIDEN.
  Query Match 6.8%; Score 81.5; DB 2; Length 438;
  Best Local Similarity 24.8%; Pred. No. 3.8;
RESULT 694
ID AAB92924 standard; protein; 519 AA.
DE Human protein sequence SEQ ID NO:11574.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
  Query Match 6.8%; Score 81.5; DB 4; Length 519;
  Best Local Similarity 22.6%; Pred. No. 4.8;
RESULT 695
ID ADE28193 standard; protein; 577 AA.
DE Human MDDT protein - SEQ ID 43.
PN WO2003046152-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match 6.8%; Score 81.5; DB 7; Length 577;
  Best Local Similarity 22.6%; Pred. No. 5.6;
RESULT 696
ID ADN23155 standard; protein; 529 AA.
DE Bacterial polypeptide #5808.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
  Query Match 6.8%; Score 81; DB 8; Length 529;
  Best Local Similarity 23.1%; Pred. No. 5.7;
RESULT 697
ID ADN23156 standard; protein; 529 AA.
DE Bacterial polypeptide #5809.
PN US2003233675-A1.

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PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.8%; Score 81; DB 8; Length 529;
RESULT 698 23.1%; Pred. No. 5.7;
ID AAG53771 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68491.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.7%; Score 80.5; DB 3; Length 322;
RESULT 699 32.7%; Pred. No. 3.3;
ID AAG5639 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29783.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.7%; Score 80.5; DB 3; Length 322;
RESULT 700 32.7%; Pred. No. 3.3;
ID AAG53746 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68457.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.7%; Score 80.5; DB 3; Length 322;
RESULT 701 32.7%; Pred. No. 3.3;
ID ABO63194 standard; protein; 350 AA.
DE Klebsiella pneumoniae polypeptide seqid 9711.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 6.7%; Score 80.5; DB 7; Length 350;
RESULT 702 31.8%; Pred. No. 3.7;
ID ABB48552 standard; protein; 463 AA.
DE Listeria monocytogenes protein #1256.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 6.7%; Score 80.5; DB 5; Length 463;
RESULT 703 19.0%; Pred. No. 5.4;
ID ABU30306 standard; protein; 463 AA.
DE Protein encoded by Prokaryotic essential gene #18563.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.7%; Score 80.5; DB 6; Length 463;
RESULT 704 19.0%; Pred. No. 5.4;
ID ADD43870 standard; protein; 536 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID NO 165.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 6.7%; Score 80.5; DB 7; Length 536;
RESULT 705 25.2%; Pred. No. 6.6;
ID AEA19162 standard; protein; 536 AA.
DE Chlamydia trachomatis protein - SEQ ID 165.
PN US2005106162-A1.
PD 19-MAY-2005.
PA (GRAN/) GRANDI G.
PA (RATT/) RATTI G.
Query Match
Best Local Similarity 6.7%; Score 80.5; DB 9; Length 536;
RESULT 706 25.2%; Pred. No. 6.6;
ID ADC42920 standard; protein; 891 AA.
DE Vaccinia Virus Major Core protein P4a precursor.

PN WO2003017943-A2.
PD 06-MAR-2003.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match
Best Local Similarity 6.7%; Score 80.5; DB 7; Length 891;
RESULT 707 23.3%; Pred. No. 13;
ID ABB92830 standard; protein; 1780 AA.
DE Herbicidally active polypeptide SEQ ID NO 2041.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.7%; Score 80.5; DB 5; Length 1780;
RESULT 708 20.8%; Pred. No. 35;
ID ABE31016 standard; protein; 1780 AA.
DE Arabidopsis thaliana glucan synthase-like protein-5.
PN WO200511215-A2.
PD 24-NOV-2005.
PA (BADI) BASF PLANT SCI GMBH.
Query Match
Best Local Similarity 6.7%; Score 80.5; DB 9; Length 1780;
RESULT 709 20.8%; Pred. No. 35;
ID AAB54399 standard; protein; 144 AA.
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:851.
PN WO200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.7%; Score 80; DB 3; Length 144;
RESULT 710 25.4%; Pred. No. 1.2;
ID AAM39952 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 3097.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.7%; Score 80; DB 4; Length 238;
RESULT 711 22.5%; Pred. No. 2.5;
ID ADM04473 standard; protein; 238 AA.
DE Human protein of the invention SEQ ID NO:3158.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 6.7%; Score 80; DB 7; Length 238;
RESULT 712 22.5%; Pred. No. 2.5;
ID AEC87403 standard; protein; 238 AA.
DE Human cDNA clone protein D90ST20002780, SEQ ID 3158.
PN EPI580263-A1.
PD 28-SEP-2005.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 6.7%; Score 80; DB 9; Length 238;
RESULT 713 22.5%; Pred. No. 2.5;
ID AAM41738 standard; protein; 249 AA.
DE Human polypeptide SEQ ID NO 6669.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.7%; Score 80; DB 4; Length 249;
RESULT 714 22.5%; Pred. No. 2.6;
ID AAR77844 standard; protein; 309 AA.
DE Molasses toxicity resistance protein RTM1.
PN WO9514774-A2.
PD 01-JUN-1995.
PA (CNRS) CENT NAT RECH SCI.
Query Match
Best Local Similarity 6.7%; Score 80; DB 2; Length 309;
RESULT 715 28.0%; Pred. No. 3.5;
ID ABM67388 standard; protein; 330 AA.
DE Photorhabdus luminescens protein sequence #485.
PN WO200294867-A2.

PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.7%; Score 80; DB 6; Length 330;
Best Local Similarity 24.6%; Pred. No. 3.9;
RESULT 716
ID AAE03831 standard; protein; 360 AA.
DE Human gene 14 encoded secreted protein HDQFN31, SEQ ID NO: 77.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 80; DB 4; Length 360;
Best Local Similarity 22.5%; Pred. No. 4.4;
RESULT 717
ID ABG64559 standard; protein; 360 AA.
DE Human albumin fusion protein #1234.
PN WO200171737-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 80; DB 5; Length 360;
Best Local Similarity 22.5%; Pred. No. 4.4;
RESULT 718
ID ADL77826 standard; protein; 360 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1308.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 6.7%; Score 80; DB 8; Length 360;
Best Local Similarity 22.5%; Pred. No. 4.4;
RESULT 719
ID ADX66260 standard; protein; 516 AA.
DE Plant full length insert polypeptide seqid 37103.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 6.7%; Score 80; DB 8; Length 516;
Best Local Similarity 20.0%; Pred. No. 7.2;
RESULT 720
ID ABU25554 standard; protein; 365 AA.
DE Protein encoded by Prokaryotic essential gene #11081.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 79.5; DB 6; Length 365;
Best Local Similarity 21.2%; Pred. No. 5.1;
RESULT 721
ID AAR58703 standard; protein; 406 AA.
DE HCMV IE-exon-4 subunit.
PN WO9417810-A1.
PD 18-AUG-1994.
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
Query Match 6.7%; Score 79.5; DB 2; Length 406;
Best Local Similarity 19.3%; Pred. No. 5.9;
RESULT 722
ID AAW27275 standard; protein; 406 AA.
DE Human cytomegalovirus immediate-early exon 4 product.
PN WO9740165-A1.
PD 30-OCT-1997.
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
Query Match 6.7%; Score 79.5; DB 2; Length 406;
Best Local Similarity 19.3%; Pred. No. 5.9;
RESULT 723
ID ABB58483 standard; protein; 638 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2241.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 6.7%; Score 79.5; DB 4; Length 638;
Best Local Similarity 20.5%; Pred. No. 11;
RESULT 724
ID AAE13277 standard; protein; 723 AA.
DE Human transporters and ion channels (TRICH) -4.
PN WO200177174-A2.
PD 18-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.7%; Score 79.5; DB 5; Length 723;
Best Local Similarity 18.0%; Pred. No. 13;
RESULT 725
ID ADL12774 standard; protein; 723 AA.
DE Human steroid-induced C3A liver cell protein #80.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.7%; Score 79.5; DB 8; Length 723;
Best Local Similarity 18.0%; Pred. No. 13;
RESULT 726
ID AAW20696 standard; protein; 121 AA.
DE H. Pylori secreted or periplasmic protein 05ae20220orf50.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.6%; Score 79; DB 2; Length 121;
Best Local Similarity 21.4%; Pred. No. 1.3;
RESULT 727
ID ABB60462 standard; protein; 323 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8178.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.6%; Score 79; DB 4; Length 323;
Best Local Similarity 18.8%; Pred. No. 4.9;
RESULT 728
ID AEB41478 standard; protein; 356 AA.
DE L. pneumophila protein SEQ ID NO 5810.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.6%; Score 79; DB 9; Length 356;
Best Local Similarity 23.0%; Pred. No. 5.6;
RESULT 729
ID AEB38189 standard; protein; 358 AA.
DE L. pneumophila protein SEQ ID NO 2521.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.6%; Score 79; DB 9; Length 358;
Best Local Similarity 23.0%; Pred. No. 5.7;
RESULT 730
ID ABR58610 standard; protein; 1531 AA.
DE Human cancer related protein SEQ ID NO:267.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.6%; Score 79; DB 6; Length 1531;
Best Local Similarity 24.3%; Pred. No. 43;
RESULT 731
ID ADE31753 standard; protein; 1531 AA.
DE Human S9590 protein #SEQ ID 110.
PN WO2003065984-A2.
PD 14-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.6%; Score 79; DB 7; Length 1531;
Best Local Similarity 24.3%; Pred. No. 43;
RESULT 732

ID AEF11993 standard; protein; 1531 AA.
DE Human heart alpha-kinase protein SEQ ID NO 2.
PN WO2005124359-A2.
PD 29-DEC-2005.
PA (META-) METABOLEX INC.
Query Match 6.6%; Score 79; DB 10; Length 1531;
Best Local Similarity 24.3%; Pred. No. 43;
RESULT 733
ID AEF11995 standard; protein; 1536 AA.
DE Human heart alpha-kinase Metabolex variant protein SEQ ID NO 4.
PN WO2005124359-A2.
PD 29-DEC-2005.
PA (META-) METABOLEX INC.
Query Match 6.6%; Score 79; DB 10; Length 1536;
Best Local Similarity 24.3%; Pred. No. 43;
RESULT 734
ID ABU62069 standard; protein; 1597 AA.
DE Human heart alpha-kinase (HK).
PN US2002177205-A1.
PD 28-NOV-2002.
PA (RYAZ/) RYAZANOV A.
Query Match 6.6%; Score 79; DB 6; Length 1597;
Best Local Similarity 24.3%; Pred. No. 45;
RESULT 735
ID ABU62070 standard; protein; 1597 AA.
DE Mouse heart alpha-kinase (HK).
PN US2002177205-A1.
PD 28-NOV-2002.
PA (RYAZ/) RYAZANOV A.
Query Match 6.6%; Score 79; DB 6; Length 1597;
Best Local Similarity 24.3%; Pred. No. 45;
RESULT 736
ID AB055689 standard; protein; 135 AA.
DE Human genome derived single exon protein #1923.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 6.6%; Score 78.5; DB 8; Length 135;
Best Local Similarity 59.4%; Pred. No. 1.7;
RESULT 737
ID ADU02890 standard; protein; 165 AA.
DE Novel human polypeptide seqid 1357.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 6.6%; Score 78.5; DB 8; Length 165;
Best Local Similarity 24.6%; Pred. No. 2.2;
RESULT 738
ID AEB38367 standard; protein; 205 AA.
DE L. pneumophila protein SEQ ID NO 2699.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCT.
Query Match 6.6%; Score 78.5; DB 9; Length 205;
Best Local Similarity 18.3%; Pred. No. 3;
RESULT 739
ID ADB10816 standard; protein; 228 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:4244.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 6.6%; Score 78.5; DB 6; Length 228;
Best Local Similarity 22.5%; Pred. No. 3.5;
RESULT 740
ID ABU36298 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #21825.
PN WO200277183-A2.
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.
Query Match 6.6%; Score 78.5; DB 6; Length 239;
Best Local Similarity 23.4%; Pred. No. 3.7;
RESULT 741
ID ADU27174 standard; protein; 626 AA.
DE Human TRICH-6, SEQ ID 6.
PN WO2004013293-A2.
PD 12-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 626;
Best Local Similarity 18.0%; Pred. No. 14;
RESULT 742
ID ABM84879 standard; protein; 648 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5128.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 648;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 743
ID ABM84877 standard; protein; 668 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5126.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 668;
Best Local Similarity 18.0%; Pred. No. 15;
RESULT 744
ID ABP29904 standard; protein; 669 AA.
DE Streptococcus polypeptide SEQ ID NO 8984.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.6%; Score 78.5; DB 5; Length 669;
Best Local Similarity 23.5%; Pred. No. 15;
RESULT 745
ID ABP28724 standard; protein; 669 AA.
DE Streptococcus polypeptide SEQ ID NO 6624.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.6%; Score 78.5; DB 5; Length 669;
Best Local Similarity 23.5%; Pred. No. 15;
RESULT 746
ID ADI21047 standard; protein; 703 AA.
DE Novel human protein #22.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 78.5; DB 7; Length 703;
Best Local Similarity 18.0%; Pred. No. 17;
RESULT 747
ID ABM84882 standard; protein; 711 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5131.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 711;
Best Local Similarity 18.0%; Pred. No. 17;
RESULT 748
ID ABP52105 standard; protein; 723 AA.
DE Homo sapiens ABC transporter ABCB9 protein SEQ ID NO:57.
PN EPI217066-A1.
PD 26-JUN-2002.
PA (UYGE-) UNIV GENT.
Query Match 6.6%; Score 78.5; DB 5; Length 723;
Best Local Similarity 18.0%; Pred. No. 17;
RESULT 749
ID ADQ97094 standard; protein; 723 AA.
DE Human cancer associated sequence HP1-10-005, SEQ ID 70.
PN WO2004060304-A2.

PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.5%; Score 78.5; DB 8; Length 723;
Best Local Similarity 18.0%; Pred. No. 17;
RESULT 750
ID AAE02437 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein.
PN W0200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 751
ID AAE02441 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein mutant K54SR.
PN W0200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 752
ID AAE02442 standard; protein; 766 AA.
DE Human ATP binding cassette, ABCB9 transporter protein mutant D667N.
PN W0200140305-A1.
PD 07-JUN-2001.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 753
ID AAG67163 standard; protein; 766 AA.
DE Amino acid sequence of a human 3894 transporter polypeptide.
PN W0200164875-A2.
PD 07-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 754
ID AAG79246 standard; protein; 766 AA.
DE Amino acid sequence of a human TAP-like (HUTAPL) polypeptide.
PN W0200173018-A2.
PD 04-OCT-2001.
PA (MERE-) MERCK PATENT GMBH.
Query Match 6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 755
ID ABB98345 standard; protein; 766 AA.
DE Human ABC transporter ABCB9 SEQ ID NO 6.
PN W0200264781-A2.
PD 22-AUG-2002.
PA (ACTI-) ACTIVE PASS PHARM INC.
Query Match 6.6%; Score 78.5; DB 5; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 756
ID AAE21170 standard; protein; 766 AA.
DE Human TRICH-14 protein.
PN W0200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.6%; Score 78.5; DB 5; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 757
ID AAE097096 standard; protein; 766 AA.
DE Human cancer associated sequence HP2-10-005, SEQ ID 72.
PN W02004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.6%; Score 78.5; DB 8; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 758
ID AAG20805 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23131.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 6.5%; Score 78; DB 3; Length 377;
Best Local Similarity 23.8%; Pred. No. 8;
RESULT 759
ID AAG20804 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23130.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 78; DB 3; Length 442;
Best Local Similarity 23.8%; Pred. No. 10;
RESULT 760
ID AAU35545 standard; protein; 471 AA.
DE Haemophilus influenzae cellular proliferation protein #186.
PN W0200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 78; DB 4; Length 471;
Best Local Similarity 25.0%; Pred. No. 11;
RESULT 761
ID ABU30411 standard; protein; 471 AA.
DE Protein encoded by Prokaryotic essential gene #15938.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 78; DB 6; Length 471;
Best Local Similarity 25.0%; Pred. No. 11;
RESULT 762
ID AAG20803 standard; protein; 489 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23129.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 78; DB 3; Length 489;
Best Local Similarity 23.8%; Pred. No. 11;
RESULT 763
ID ABB49039 standard; protein; 269 AA.
DE Listeria monocytogenes protein #1743.
PN W0200177335-A2.
PD 18-OCT-2001.
PA (INSP-) INST PASTEUR.
Query Match 6.5%; Score 77.5; DB 5; Length 269;
Best Local Similarity 22.0%; Pred. No. 5.7;
RESULT 764
ID ABG17374 standard; protein; 280 AA.
DE Novel human diagnostic protein #17365.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 77.5; DB 4; Length 280;
Best Local Similarity 21.9%; Pred. No. 6.1;
RESULT 765
ID ABO00771 standard; protein; 280 AA.
DE Polypeptide encoded by novel human contig #22.
PN W02003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 77.5; DB 6; Length 280;
Best Local Similarity 21.9%; Pred. No. 6.1;
RESULT 766
ID ABU4889 standard; protein; 327 AA.
DE Protein encoded by Prokaryotic essential gene #34416.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 77.5; DB 6; Length 327;
Best Local Similarity 24.8%; Pred. No. 7.5;
RESULT 767
ID AAW13576 standard; protein; 438 AA.
DE Mouse Batten disease polypeptide CLN3 homologue.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 6.5%; Score 77.5; DB 2; Length 438;
Best Local Similarity 27.6%; Pred. No. 11;

RESULT 768
ID ADG42965 standard; protein; 491 AA.
DE Bacterial polypeptide #21395.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.5%; Score 77.5; DB 8; Length 491;
Best Local Similarity 22.6%; Pred. No. 13;
RESULT 769
ID ADC42919 standard; protein; 892 AA.
DE Variola smallpox virus A10L.
PN WO2003017943-A2.
PD 06-MAR-2003.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 6.5%; Score 77.5; DB 7; Length 892;
Best Local Similarity 22.7%; Pred. No. 30;
RESULT 770
ID AEP63571 standard; protein; 930 AA.
DE Ostreococcus tauri phospholipase 2 protein.
PN WO2006008099-A2.
PD 26-JAN-2006.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 6.5%; Score 77.5; DB 10; Length 930;
Best Local Similarity 19.7%; Pred. No. 32;
RESULT 771
ID AAR88413 standard; protein; 353 AA.
DE High-affinity melatonin-1a receptor.
PN WO9535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 6.4%; Score 77; DB 2; Length 353;
Best Local Similarity 22.1%; Pred. No. 9.6;
RESULT 772
ID AAM23958 standard; protein; 353 AA.
DE Mouse melatonin la receptor.
PN WO9803549-A1.
PD 29-JAN-1998.
PA (GHHO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 77; DB 2; Length 353;
Best Local Similarity 22.1%; Pred. No. 9.6;
RESULT 773
ID ABB07571 standard; protein; 353 AA.
DE Mouse melatonin la (Mella) receptor.
PN USG326526-B1.
PD 04-DEC-2001.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (GHHO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 77; DB 5; Length 353;
Best Local Similarity 22.1%; Pred. No. 9.6;
RESULT 774
ID ADO29553 standard; protein; 353 AA.
DE Mouse GPCR MTNR1A, SEQ ID NO:655.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.4%; Score 77; DB 8; Length 353;
Best Local Similarity 22.1%; Pred. No. 9.6;
RESULT 775
ID ADM25403 standard; protein; 383 AA.
DE Hyperthermophile Methanopyrus kandleri protein #9.
PN WO2003076575-A2.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
Query Match 6.4%; Score 77; DB 7; Length 383;
Best Local Similarity 24.8%; Pred. No. 11;
RESULT 776
ID ADQ95948 standard; protein; 490 AA.
DE T cell activation associated protein #63.

PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.4%; Score 77; DB 8; Length 490;
Best Local Similarity 19.5%; Pred. No. 15;
RESULT 777
ID ADQ96002 standard; protein; 490 AA.
DE T cell activation associated protein #90.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.4%; Score 77; DB 8; Length 490;
Best Local Similarity 19.5%; Pred. No. 15;
RESULT 778
ID AAG42521 standard; protein; 648 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53040.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 648;
Best Local Similarity 20.4%; Pred. No. 22;
RESULT 779
ID ABUL6172 standard; protein; 650 AA.
DE Protein encoded by Prokaryotic essential gene #1699.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 77; DB 6; Length 650;
Best Local Similarity 27.5%; Pred. No. 22;
RESULT 780
ID ABM72713 standard; protein; 650 AA.
DE Staphylococcus aureus protein #1953.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.4%; Score 77; DB 6; Length 650;
Best Local Similarity 27.5%; Pred. No. 22;
RESULT 781
ID AAG42520 standard; protein; 690 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53039.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 690;
Best Local Similarity 20.4%; Pred. No. 24;
RESULT 782
ID AAG42519 standard; protein; 728 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53038.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 728;
Best Local Similarity 20.4%; Pred. No. 26;
RESULT 783
ID AAG32549 standard; protein; 805 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39287.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 805;
Best Local Similarity 20.4%; Pred. No. 30;
RESULT 784
ID AAG32548 standard; protein; 847 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39286.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 847;
Best Local Similarity 20.4%; Pred. No. 32;
RESULT 785
ID AAG32547 standard; protein; 991 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39285.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 991;
Best Local Similarity 20.4%; Pred. No. 40;
RESULT 786
ID ABP52133 standard; protein; 1025 AA.

DE Plasmodium falciparum multidrug resistance protein SEQ ID NO: 85.
PN EP1217066-A1.
PA (UYGE-) UNIV GENT.
Query Match 6.4%; Score 77; DB 5; Length 1025;
Best Local Similarity 20.6%; Pred. No. 42;
RESULT 787
ID AAG42381 standard; protein; 1047 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52849.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1047;
Best Local Similarity 20.4%; Pred. No. 43;
RESULT 788
ID AAG42380 standard; protein; 1191 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52848.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1191;
Best Local Similarity 20.4%; Pred. No. 52;
RESULT 789
ID AAG42379 standard; protein; 1202 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52847.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1202;
Best Local Similarity 20.4%; Pred. No. 52;
RESULT 790
ID AAR29527 standard; protein; 2510 AA.
DE HCV antigen T7N1-30.
PN EP518313-A2.
PD 16-DEC-1992.
PA (MITU) MITSUBISHI KASEI CORP.
Query Match 6.4%; Score 77; DB 2; Length 2510;
Best Local Similarity 22.5%; Pred. No. 1.5e+02;
RESULT 791
ID ADX40818 standard; protein; 3010 AA.
DE HCV polymerase protein #41.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMMUNE INC.
Query Match 6.4%; Score 77; DB 9; Length 3010;
Best Local Similarity 22.5%; Pred. No. 1.9e+02;
RESULT 792
ID ADX40816 standard; protein; 3010 AA.
DE HCV polymerase protein #39.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMMUNE INC.
Query Match 6.4%; Score 77; DB 9; Length 3010;
Best Local Similarity 22.5%; Pred. No. 1.9e+02;
RESULT 793
ID ADT56855 standard; protein; 195 AA.
DE Plant polypeptide, SEQ ID 6932.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 6.4%; Score 76.5; DB 8; Length 195;
Best Local Similarity 25.8%; Pred. No. 4.8;
RESULT 794
ID ADF74966 standard; protein; 249 AA.
DE Human 164-1h protein (SeqID 25).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.4%; Score 76.5; DB 8; Length 249;
Best Local Similarity 23.3%; Pred. No. 6.7;
RESULT 795
ID ADC01137 standard; protein; 278 AA.
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 1181.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.

Query Match 6.4%; Score 76.5; DB 7; Length 278;
Best Local Similarity 28.5%; Pred. No. 7.9;
RESULT 796
ID ABO65827 standard; protein; 435 AA.
DE Klebsiella pneumoniae polypeptide seqid 12344.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.4%; Score 76.5; DB 7; Length 435;
Best Local Similarity 21.8%; Pred. No. 15;
RESULT 797
ID ADF74969 standard; protein; 481 AA.
DE Human 164-1h protein (SeqID 28).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.4%; Score 76.5; DB 8; Length 481;
Best Local Similarity 23.3%; Pred. No. 17;
RESULT 798
ID AAR90765 standard; protein; 494 AA.
DE Human K+ channel 2 mature protein.
PN WO9603415-A1.
PD 08-FEB-1996.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76.5; DB 2; Length 494;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 799
ID AAW42996 standard; protein; 494 AA.
DE Putative mature potassium channel 2 protein..
PN US5710019-A.
PD 20-JAN-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76.5; DB 2; Length 494;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 800
ID ABP58356 standard; protein; 494 AA.
DE Human potassium channel subunit Kv5.1.
PN WO200296944-A2.
PD 05-DEC-2002.
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match 6.4%; Score 76.5; DB 6; Length 494;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 801
ID ADC99155 standard; protein; 494 AA.
DE Human mature K+ channel 2 protein.
PN US2003092895-A1.
PD 15-MAY-2003.
PA (LIYY/) LI Y.
PA (ADAM/) ADAMS M D.
PA (WHIT/) WHITE O R.
Query Match 6.4%; Score 76.5; DB 7; Length 494;
Best Local Similarity 21.3%; Pred. No. 17;
RESULT 802
ID AAW20085 standard; protein; 509 AA.
DE Helicobacter pylori cytoplasmic protein, 10009666.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.4%; Score 76.5; DB 2; Length 509;
Best Local Similarity 19.2%; Pred. No. 18;
RESULT 803
ID ADQ07984 standard; protein; 526 AA.
DE Human hypothetical protein FLJ20371-encoding cDNA.
PN WO2004061123-A2.
PD 22-JUL-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 6.4%; Score 76.5; DB 8; Length 526;
Best Local Similarity 15.7%; Pred. No. 19;
RESULT 804
ID ADP25065 standard; protein; 526 AA.
DE PRO polypeptide SEQ ID NO: 2243.
PN WO2004041170-A2.
PD 21-MAY-2004.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 8; Length 526;
RESULT 805
ID AD06638 standard; protein; 526 AA.
DE Novel bronchial cancer-associated human protein SeqID864.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 8; Length 526;
RESULT 806
ID AD063957 standard; protein; 555 AA.
DE Human protein encoded by clone ASTR020053430.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 7; Length 555;
RESULT 807
ID ABB08159 standard; protein; 570 AA.
DE Human cytoskeleton-associated protein (CSAP)-3 (ID: 7091536CD1).
PN WO200242330-A2.
PD 30-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 5; Length 570;
RESULT 808
ID AAW20918 standard; protein; 593 AA.
DE H. pylori transporter protein, 14gpi2015orf14.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 2; Length 593;
RESULT 809
ID ADN46225 standard; protein; 615 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID103.
PN WO200402736-A1.
PD 18-MAR-2004.
PA (NTSC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 8; Length 615;
RESULT 810
ID ADN21126 standard; protein; 2539 AA.
DE Bacterial polypeptide #3779.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 8; Length 2539;
RESULT 811
ID ADH8107 standard; protein; 195 AA.
DE Enterococcus faecalis polypeptide #2587.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 6.4%; Score 76; DB 7; Length 195;
RESULT 812
ID AAG09592 standard; protein; 274 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7586.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 76; DB 3; Length 274;

Best Local Similarity 26.7%; Pred. No. 8.8;
RESULT 813
ID AAG09591 standard; protein; 287 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7585.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 76; DB 3; Length 287;
RESULT 814
ID ADQ96244 standard; protein; 366 AA.
DE T cell activation associated protein #211.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 6.4%; Score 76; DB 8; Length 366;
RESULT 815
ID ADQ96246 standard; protein; 366 AA.
DE T cell activation associated protein #212.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 6.4%; Score 76; DB 8; Length 366;
RESULT 816
ID ABB89424 standard; protein; 456 AA.
DE Human polypeptide SEQ ID NO 1800.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.4%; Score 76; DB 5; Length 456;
RESULT 817
ID AAB53400 standard; protein; 557 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:940.
PN WO20005351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.4%; Score 76; DB 3; Length 557;
RESULT 818
ID AAY44945 standard; protein; 593 AA.
DE Wheat sulphate permease-2.
PN WO200004154-A2.
PD 27-JAN-2000.
PA (DUPO) DU FONT DE NEMOURS & CO S I.
Query Match
Best Local Similarity 6.4%; Score 76; DB 3; Length 593;
RESULT 819
ID ADN22849 standard; protein; 1402 AA.
DE Bacterial polypeptide #5502.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.4%; Score 76; DB 8; Length 1402;
RESULT 820
ID AEF10990 standard; protein; 1783 AA.
DE C. elegans VDCC alpha 1 subunit, Cav2.1.
PN US2005288489-A1.
PD 29-DEC-2005.
PA (HIRS/) HIRSCH J A.
Query Match
Best Local Similarity 6.4%; Score 76; DB 10; Length 1783;
RESULT 821
ID ADN23383 standard; protein; 1917 AA.
DE Bacterial polypeptide #6036.
PN US2003233675-A1.
PD 18-DEC-2003.

PA (CAOV/) CAO Y. 6.4%; Score 76; DB 8; Length 1917;
 PA (HINK/) HINKLE G J. 18.5%; Pred. No. 1.3e+02;
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 6.4%; Score 76; DB 8; Length 1917;
 Best Local Similarity 18.5%; Pred. No. 1.3e+02;
 RESULT 822
 ID ADX40794 standard; protein; 3010 AA.
 DE HCV polymerase protein #17.
 PN WO2005012502-A2.
 PD 10-FEB-2005.
 PA (EPIN-) EPIMMUNE INC.
 Query Match 6.4%; Score 76; DB 9; Length 3010;
 Best Local Similarity 25.4%; Pred. No. 2.5e+02;
 RESULT 823
 ID ADX40791 standard; protein; 3010 AA.
 DE HCV polymerase protein #14.
 PN WO2005012502-A2.
 PD 10-FEB-2005.
 PA (EPIN-) EPIMMUNE INC.
 Query Match 6.4%; Score 76; DB 9; Length 3010;
 Best Local Similarity 25.4%; Pred. No. 2.5e+02;
 RESULT 824
 ID ADX40792 standard; protein; 3010 AA.
 DE HCV polymerase protein #15.
 PN WO2005012502-A2.
 PD 10-FEB-2005.
 PA (EPIM-) EPIMMUNE INC.
 Query Match 6.4%; Score 76; DB 9; Length 3010;
 Best Local Similarity 26.9%; Pred. No. 2.5e+02;
 RESULT 825
 ID ABB63150 standard; protein; 228 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 16242.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 6.3%; Score 75.5; DB 4; Length 228;
 Best Local Similarity 21.8%; Pred. No. 7.8;
 RESULT 826
 ID ADK46533 standard; protein; 263 AA.
 DE Streptococcus pneumoniae protein, Seq ID No 3148.
 PN US6699703-B1.
 PD 02-MAR-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 6.3%; Score 75.5; DB 8; Length 263;
 Best Local Similarity 18.0%; Pred. No. 9.5;
 RESULT 827
 ID ADM92206 standard; protein; 263 AA.
 DE S pneumoniae antigenic protein sequence SeqID403.
 PN WO2004020609-A2.
 PD 11-MAR-2004.
 PA (TUFT) UNIV TUFTS.
 Query Match 6.3%; Score 75.5; DB 8; Length 263;
 Best Local Similarity 18.0%; Pred. No. 9.5;
 RESULT 828
 ID AAY81619 standard; protein; 264 AA.
 DE Streptococcus pneumoniae type 4 protein sequence #119.
 PN WO200006737-A2.
 PD 10-FEB-2000.
 PA (MICR-) MICROBIAL TECHNIQS LTD.
 Query Match 6.3%; Score 75.5; DB 3; Length 264;
 Best Local Similarity 18.0%; Pred. No. 9.6;
 RESULT 829
 ID ADR96242 standard; protein; 264 AA.
 DE Novel S. pneumoniae protein sequence, SEQ ID 4877.
 PN US6800744-B1.
 PD 05-OCT-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 6.3%; Score 75.5; DB 8; Length 264;
 Best Local Similarity 18.0%; Pred. No. 9.6;
 RESULT 830
 ID AEA60112 standard; protein; 264 AA.

DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:4877.
 PN US2005136404-A1.
 PD 23-JUN-2005.
 PA (DOUC/) DOUCETTE-STAMM L A.
 PA (BUSH/) BUSH D.
 Query Match 6.3%; Score 75.5; DB 9; Length 264;
 Best Local Similarity 18.0%; Pred. No. 9.6;
 RESULT 831
 ID ABU02182 standard; protein; 276 AA.
 DE S. pneumoniae type 4 strain protein from coding region #1759.
 PN WO200277021-A2.
 PD 03-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Query Match 6.3%; Score 75.5; DB 6; Length 276;
 Best Local Similarity 18.0%; Pred. No. 10;
 RESULT 832
 ID ABG93285 standard; protein; 342 AA.
 DE C. albicans BAX-associated protein fragment SEQ ID 528.
 PN WO200264766-A2.
 PD 22-AUG-2002.
 PA (JANC) JANSSEN PHARM NV.
 Query Match 6.3%; Score 75.5; DB 5; Length 342;
 Best Local Similarity 21.9%; Pred. No. 14;
 RESULT 833
 ID AAB15936 standard; protein; 352 AA.
 DE E. coli proliferation associated protein sequence SEQ ID NO:293.
 PN WO200044906-A2.
 PD 03-AUG-2000.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.3%; Score 75.5; DB 3; Length 352;
 Best Local Similarity 31.7%; Pred. No. 14;
 RESULT 834
 ID ADH51470 standard; protein; 363 AA.
 DE Rat MT1 receptor amino acid sequence #SEQ ID 2.
 PN FR2835847-A1.
 PD 15-AUG-2003.
 PA (SERV-) LES LAB SERVIER SA.
 Query Match 6.3%; Score 75.5; DB 7; Length 363;
 Best Local Similarity 23.5%; Pred. No. 15;
 RESULT 835
 ID AAU03851 standard; protein; 397 AA.
 DE G protein-coupled receptor-like (GPCR-like) receptor protein #23.
 PN WO200138533-A2.
 PD 31-MAY-2001.
 PA (PHAA) PHARMACIA & UPJOHN.
 Query Match 6.3%; Score 75.5; DB 4; Length 397;
 Best Local Similarity 19.1%; Pred. No. 17;
 RESULT 836
 ID ADU92092 standard; protein; 415 AA.
 DE Escherichia coli tnaB protein.
 PN EP148410-A1.
 PD 08-DEC-2004.
 PA (AJIN) AJINOMOTO KK.
 Query Match 6.3%; Score 75.5; DB 9; Length 415;
 Best Local Similarity 20.5%; Pred. No. 18;
 RESULT 837
 ID AEB41698 standard; protein; 430 AA.
 DE L. pneumophila protein SEQ ID NO 6030.
 PN WO2005049642-A2.
 PD 02-JUN-2005.
 PA (INSP) INST PASTEUR.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 6.3%; Score 75.5; DB 9; Length 430;
 Best Local Similarity 25.5%; Pred. No. 19;
 RESULT 838
 ID AAU03852 standard; protein; 433 AA.
 DE G protein-coupled receptor-like (GPCR-like) receptor protein #24.
 PN WO200138533-A2.
 PD 31-MAY-2001.
 PA (PHAA) PHARMACIA & UPJOHN.

Query Match
Best Local Similarity 6.3%; Score 75.5; DB 4; Length 433;
RESULT 839
ID AEB38437 standard; protein; 436 AA.
DE L. pneumophila protein SEQ ID NO 2769.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 6.3%; Score 75.5; DB 9; Length 436;
RESULT 840
ID ADS24239 standard; protein; 463 AA.
DE Bacterial polypeptide #13272.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.3%; Score 75.5; DB 8; Length 463;
RESULT 841
ID ADO29507 standard; protein; 471 AA.
DE Mouse GPCR HTR2A, SEQ ID NO:609.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 6.3%; Score 75.5; DB 8; Length 471;
RESULT 842
ID AAU03820 standard; protein; 499 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #19.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match
Best Local Similarity 6.3%; Score 75.5; DB 4; Length 499;
RESULT 843
ID ADM72132 standard; protein; 392 AA.
DE Human NTRAN polypeptide (clone ID 7524555CD1).
PN WO2004022705-A2.
PD 18-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 6.3%; Score 75; DB 8; Length 392;
RESULT 844
ID ARM90212 standard; protein; 404 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:8934.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 6.3%; Score 75; DB 7; Length 404;
RESULT 845
ID AEB39222 standard; protein; 418 AA.
DE L. pneumophila protein SEQ ID NO 3554.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 6.3%; Score 75; DB 9; Length 418;
RESULT 846
ID AEB35772 standard; protein; 437 AA.
DE L. pneumophila protein SEQ ID NO 104.
PN WO2005049642-A2.
PD 02-JUN-2005.

PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 6.3%; Score 75; DB 9; Length 437;
RESULT 847
ID AAU45917 standard; protein; 445 AA.
DE Propionibacterium acnes immunogenic protein #6813.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 6.3%; Score 75; DB 4; Length 445;
RESULT 848
ID ABM42436 standard; protein; 445 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #7112.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 6.3%; Score 75; DB 6; Length 445;
RESULT 849
ID ABM87563 standard; protein; 452 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:5809.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 6.3%; Score 75; DB 7; Length 452;
RESULT 850
ID ADA34178 standard; protein; 467 AA.
DE Acinetobacter baumannii protein #1339.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 6.3%; Score 75; DB 6; Length 467;
RESULT 851
ID ADR14597 standard; protein; 473 AA.
DE Human NF-kappaB pathway-associated protein SeqID598.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 6.3%; Score 75; DB 8; Length 473;
RESULT 852
ID ADP99138 standard; protein; 480 AA.
DE Human transporter and ion channel (TRICH) protein - SEQ ID 3.
PN WO2004048599-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 6.3%; Score 75; DB 8; Length 480;
RESULT 853
ID ADH86490 standard; protein; 549 AA.
DE Enterococcus faecalis polypeptide #970.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 6.3%; Score 75; DB 7; Length 549;
RESULT 854
ID ADX80121 standard; protein; 635 AA.
DE Plant full length insert polypeptide seqid 49487.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.

PA (CAOX/) CAO Y.
Query Match 6.3%; Score 75; DB 8; Length 635;
Best Local Similarity 25.3%; Pred. No. 37;
RESULT 855
ID AAR54066 standard; protein; 1051 AA.
DE Non-A, non-B hepatitis virus gene #4 product.
PN JP06141870-A.
PD 24-MAY-1994.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
PA (TOFU) TONEN CORP.
Query Match 6.3%; Score 75; DB 2; Length 1051;
Best Local Similarity 23.4%; Pred. No. 75;
RESULT 856
ID AAR98361 standard; protein; 1051 AA.
DE 5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).
PN JP07133291-A.
PD 23-MAY-1995.
PA (TOFU) TONEN CORP.
Query Match 6.3%; Score 75; DB 2; Length 1051;
Best Local Similarity 23.4%; Pred. No. 75;
RESULT 857
ID ADB64712 standard; protein; 1131 AA.
DE Human protein encoded by clone NT2NE20077270.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.3%; Score 75; DB 7; Length 1131;
Best Local Similarity 23.9%; Pred. No. 83;
RESULT 858
ID ABB64494 standard; protein; 2248 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20274.
PN WO200171042-A.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 75; DB 4; Length 2248;
Best Local Similarity 22.9%; Pred. No. 2.1e+02;
RESULT 859
ID ADG20763 standard; protein; 2248 AA.
DE Drosophila melanogaster rutabaga protein SEQ ID NO:2.
PN WO2003103704-A2.
PD 18-DEC-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 6.3%; Score 75; DB 8; Length 2248;
Best Local Similarity 22.9%; Pred. No. 2.1e+02;
RESULT 860
ID ADQ89656 standard; protein; 2248 AA.
DE Antagonist of cell cycle progression polypeptide #43.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 6.3%; Score 75; DB 8; Length 2248;
Best Local Similarity 22.9%; Pred. No. 2.1e+02;
RESULT 861
ID ADX40796 standard; protein; 3010 AA.
DE HCV polymerase protein #19.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMUNE INC.
Query Match 6.3%; Score 75; DB 9; Length 3010;
Best Local Similarity 25.4%; Pred. No. 3.2e+02;
RESULT 862
ID AAB66797 standard; protein; 200 AA.
DE Porcine reproductive and respiratory syndrome virus ORF #5 protein.
PN WO200102858-A1.
PD 11-JAN-2001.
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
PA (NATE-) INST MATERIALS RES & ENG.
Query Match 6.2%; Score 74.5; DB 4; Length 200;
Best Local Similarity 23.8%; Pred. No. 8.6;
RESULT 863
ID ADF74954 standard; protein; 256 AA.

DE Rat 164-lh protein (SeqID 13).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.2%; Score 74.5; DB 8; Length 256;
Best Local Similarity 23.3%; Pred. No. 12;
RESULT 864
ID AAR53748 standard; protein; 355 AA.
DE Seven transmembrane receptor (V28).
PN WO9412635-A2.
PD 09-JUN-1994.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 2; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 865
ID AAM48722 standard; protein; 355 AA.
DE Human V28 seven transmembrane receptor.
PN US5759804-A.
PD 02-JUN-1998.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 2; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 866
ID AAY90677 standard; protein; 355 AA.
DE Human mutant G protein-coupled receptor V28 (I230K).
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 867
ID AAY90642 standard; protein; 355 AA.
DE Human G protein-coupled receptor V28.
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 868
ID AAB21693 standard; protein; 355 AA.
DE Human 7TM receptor V28 cDNA clone protein #2.
PN US6107475-A.
PD 22-AUG-2000.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 869
ID AAB21692 standard; protein; 355 AA.
DE Human 7TM receptor V28 cDNA clone protein #1.
PN US6107475-A.
PD 22-AUG-2000.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 870
ID AAG80126 standard; protein; 355 AA.
DE Human CX3CR1 protein.
PN WO200172830-A2.
PD 04-OCT-2001.
PA (IPRP-) IPF PHARM GMBH.
PA (FORS-) FORSSMANN U.
Query Match 6.2%; Score 74.5; DB 4; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 871
ID AAB82786 standard; protein; 355 AA.
DE Human CX3C chemokine receptor 1.
PN WO200160406-A1.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PHARM INC.
PA (NOUN) UNIV NORTHWESTERN.
Query Match 6.2%; Score 74.5; DB 4; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 872

ID AAU91235 standard; protein; 355 AA.
DE Human 7 transmembrane domain receptor V28 #2.
PN US6348574-B1.
PD 19-FEB-2002.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 5; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 873
ID AAU91234 standard; protein; 355 AA.
DE Human 7 transmembrane domain receptor V28 #1.
PN US6348574-B1.
PD 19-FEB-2002.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 5; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 874
ID AAU84327 standard; protein; 355 AA.
DE Protein CX3CR1 differentially expressed in breast cancer tissue.
PN WO200210436-A2.
PD 07-FEB-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA (BAK) BAK J.
Query Match 6.2%; Score 74.5; DB 5; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 875
ID ABR58524 standard; protein; 355 AA.
DE Human chemokine (C-X3-C) receptor 1 protein.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 876
ID AQA29513 standard; protein; 355 AA.
DE Human fractalkine receptor (313) protein.
PN WO2003039475-A2.
PD 15-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 877
ID ABR7732 standard; protein; 355 AA.
DE Amino acid sequence of human chemokine receptor CX3CR1.
PN WO2003014153-A2.
PD 20-FEB-2003.
PA (TOPI-) TOPIGEN PHARM INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 878
ID ABR81882 standard; protein; 355 AA.
DE Human CX3C chemokine fractalkine receptor 1 protein SEQ ID NO:249.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 879
ID ADC22751 standard; protein; 355 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #74.
PN US6553339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 880
ID ADC22649 standard; protein; 355 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #34.
PN US6553339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 881

ID ADH14224 standard; protein; 355 AA.
DE Mutated human serotonin V28.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 882
ID ADH14122 standard; protein; 355 AA.
DE Human serotonin V28.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 883
ID ADH10680 standard; protein; 355 AA.
DE Human CX3CR1 polypeptide.
PN WO2003104484-A1.
PD 18-DEC-2003.
PA (META-) METABOLEX INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 884
ID ADO29269 standard; protein; 355 AA.
DE Human GPCR CX3CR1, SEQ ID NO:370.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 885
ID ADQ18141 standard; protein; 355 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 958.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 886
ID ADP56020 standard; protein; 355 AA.
DE Human PRO protein sequence SEQ ID NO:1996.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 887
ID ADP54585 standard; protein; 355 AA.
DE Human PRO protein sequence SEQ ID NO:561.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 888
ID ADP23931 standard; protein; 355 AA.
DE PRO polypeptide SEQ ID NO:1109.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;
RESULT 889
ID ADQ39421 standard; protein; 355 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1084.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.

Query Match 6.2%; Score 74.5; DB 8; Length 355;
 Best Local Similarity 25.8%; Pred. No. 19;
 RESULT 890
 ID ADY15644 standard; protein; 355 AA.
 DE PRO polypeptide SEQ ID NO 1450.
 PN WO2005016962-A2.
 PD 24-FEB-2005.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 74.5; DB 9; Length 355;
 Best Local Similarity 25.8%; Pred. No. 19;
 RESULT 891
 ID AED67635 standard; protein; 355 AA.
 DE Human CX3C chemokine receptor 1 (CX3CR1).
 PN WO2005103684-A2.
 PD 03-NOV-2005.
 PA (FARB) BAYER HEALTHCARE AG.
 Query Match 6.2%; Score 74.5; DB 9; Length 355;
 Best Local Similarity 25.8%; Pred. No. 19;
 RESULT 892
 ID ADQ39422 standard; protein; 362 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1085.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 6.2%; Score 74.5; DB 8; Length 362;
 Best Local Similarity 25.8%; Pred. No. 19;
 RESULT 893
 ID AAW77109 standard; protein; 471 AA.
 DE Rat 5-HT2A serotonin receptor C322K mutant.
 PN WO9838217-A1.
 PD 03-SEP-1998.
 PA (TEIT/) TEITLER M.
 PA (HERR/) HERRICK-DAVIS K.
 PA (EGAN/) EGAN C C.
 Query Match 6.2%; Score 74.5; DB 2; Length 471;
 Best Local Similarity 21.0%; Pred. No. 28;
 RESULT 894
 ID AAW77111 standard; protein; 471 AA.
 DE Rat 5-HT2A serotonin receptor C322E mutant.
 PN WO9838217-A1.
 PD 03-SEP-1998.
 PA (TEIT/) TEITLER M.
 PA (HERR/) HERRICK-DAVIS K.
 PA (EGAN/) EGAN C C.
 Query Match 6.2%; Score 74.5; DB 2; Length 471;
 Best Local Similarity 21.0%; Pred. No. 28;
 RESULT 895
 ID AAW77110 standard; protein; 471 AA.
 DE Rat 5-HT2A serotonin receptor C322R mutant.
 PN WO9838217-A1.
 PD 03-SEP-1998.
 PA (TEIT/) TEITLER M.
 PA (HERR/) HERRICK-DAVIS K.
 PA (EGAN/) EGAN C C.
 Query Match 6.2%; Score 74.5; DB 2; Length 471;
 Best Local Similarity 21.0%; Pred. No. 28;
 RESULT 896
 ID AAW77104 standard; protein; 471 AA.
 DE Rat 5-HT2A serotonin receptor.
 PN WO9838217-A1.
 PD 03-SEP-1998.
 PA (TEIT/) TEITLER M.
 PA (HERR/) HERRICK-DAVIS K.
 PA (EGAN/) EGAN C C.
 Query Match 6.2%; Score 74.5; DB 2; Length 471;
 Best Local Similarity 21.0%; Pred. No. 28;
 RESULT 897
 ID ABB07980 standard; protein; 471 AA.
 DE Rat 5-HT2 receptor sequence.
 PN US6383762-B1.
 PD 07-MAY-2002.
 PA (SYNA-) SYNAPTIC PHARM CORP.
 Query Match 6.2%; Score 74.5; DB 5; Length 471;

Best Local Similarity 21.0%; Pred. No. 28;
 RESULT 898
 ID ADF74971 standard; protein; 481 AA.
 DE Rat 164-1b protein (SeqID 30).
 PN WO2003097886-A1.
 PD 27-NOV-2003.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match 6.2%; Score 74.5; DB 8; Length 481;
 Best Local Similarity 23.3%; Pred. No. 29;
 RESULT 899
 ID AAM93692 standard; protein; 562 AA.
 DE Human polypeptide, SEQ ID NO: 3602.
 PN EP1130094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 6.2%; Score 74.5; DB 4; Length 562;
 Best Local Similarity 23.1%; Pred. No. 36;
 RESULT 900
 ID ADL31569 standard; protein; 562 AA.
 DE Human protein encoded by a full length cDNA clone SeqID 3602.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 6.2%; Score 74.5; DB 8; Length 562;
 Best Local Similarity 23.1%; Pred. No. 36;
 RESULT 901
 ID ADQ96138 standard; protein; 562 AA.
 DE T cell activation associated protein #158.
 PN WO2004058805-A2.
 PD 15-JUL-2004.
 PA (ASAH-) ASahi Kasei PHARMA CORP.
 Query Match 6.2%; Score 74.5; DB 8; Length 562;
 Best Local Similarity 23.1%; Pred. No. 36;
 RESULT 902
 ID ADR86160 standard; protein; 587 AA.
 DE Aspergillus fumigatus essential gene protein #210.
 PN WO2004057709-A2.
 PD 12-AUG-2004.
 PA (ELIT-) ELITRA PHARM INC.
 PA (ELIT-) ELITRA CANADA LTD.
 Query Match 6.2%; Score 74.5; DB 8; Length 587;
 Best Local Similarity 18.2%; Pred. No. 38;
 RESULT 903
 ID ABB62948 standard; protein; 597 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 15636.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 6.2%; Score 74.5; DB 4; Length 597;
 Best Local Similarity 27.2%; Pred. No. 39;
 RESULT 904
 ID ADX66440 standard; protein; 661 AA.
 DE Plant full length insert polypeptide seqid 37283.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOV/) CAO Y.
 Query Match 6.2%; Score 74.5; DB 8; Length 661;
 Best Local Similarity 20.4%; Pred. No. 45;
 RESULT 905
 ID ADA36878 standard; protein; 940 AA.
 DE Acinetobacter baumannii protein #4039.
 PN US6562958-B1.
 PD 13-MAY-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 6.2%; Score 74.5; DB 6; Length 940;
 Best Local Similarity 21.1%; Pred. No. 73;
 RESULT 906
 ID ABB92731 standard; protein; 1808 AA.

DE Herbicidally active polypeptide SEQ ID NO 1942.
 PN WO200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match 6.2%; Score 74.5; DB 5; Length 1808;
 Best Local Similarity 17.3%; Pred. No. 1.8e+02;
 RESULT 907
 ID AAE20477 standard; protein; 3010 AA.
 DE HCV-S1 full-length polypeptide.
 PN WO200208447-A2.
 PD 31-JAN-2002.
 PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
 PA (EHLR/) EHLRICH G.
 Query Match
 Best Local Similarity 6.2%; Score 74.5; DB 5; Length 3010;
 RESULT 908
 ID ADF07294 standard; protein; 154 AA.
 DE Bacterial polypeptide #3407.
 PN US6605709-B1.
 PD 12-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 7; Length 154;
 RESULT 909
 ID ABU70365 standard; protein; 231 AA.
 DE Human adipocyte bait protein, melatonin receptor_V4.
 PN WO200286122-A2.
 PD 31-OCT-2002.
 PA (HYBR-) HYBRIGENICS.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 6; Length 231;
 RESULT 910
 ID ABU70366 standard; protein; 231 AA.
 DE Human adipocyte bait protein, melatonin receptor_V5.
 PN WO200286122-A2.
 PD 31-OCT-2002.
 PA (HYBR-) HYBRIGENICS.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 6; Length 231;
 RESULT 911
 ID ABB54180 standard; protein; 312 AA.
 DE Lactococcus lactis protein yliG.
 PN FR2807446-A1.
 PD 12-OCT-2001.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 5; Length 312;
 RESULT 912
 ID ADS44483 standard; protein; 312 AA.
 DE Bacterial polypeptide #22913.
 PN US200233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 8; Length 312;
 RESULT 913
 ID ABU02869 standard; protein; 324 AA.
 DE S. pneumoniae type 4 strain protein from coding region #2450.
 PN WO20027021-A2.
 PD 03-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 6; Length 324;
 RESULT 914
 ID ADR94027 standard; protein; 332 AA.
 DE Novel S. pneumoniae protein sequence, SEQ ID 2662.
 PN US6800744-B1.
 PD 05-OCT-2004.

PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 8; Length 332;
 RESULT 915
 ID AEA57897 standard; protein; 332 AA.
 DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:2662.
 PN US2005136404-A1.
 PD 23-JUN-2005.
 PA (DOUC/) DOUCETTE-STAMM L A.
 PA (BUSH/) BUSH D.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 9; Length 332;
 RESULT 916
 ID ABO00448 standard; protein; 342 AA.
 DE Novel human polypeptide #35.
 PN WO2003023013-A2.
 PD 20-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 6; Length 342;
 RESULT 917
 ID AAR88412 standard; protein; 350 AA.
 DE High-affinity melatonin-1a receptor.
 PN WO9535320-A1.
 PD 28-DEC-1995.
 PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 2; Length 350;
 RESULT 918
 ID AAW15786 standard; protein; 350 AA.
 DE Melatonin receptor protein.
 PN JP09084581-A.
 PD 31-MAR-1997.
 PA (TAKE) TAKEDA CHEM IND LTD.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 2; Length 350;
 RESULT 919
 ID AAW94761 standard; protein; 350 AA.
 DE Human melatonin receptor protein mel-1a.
 PN EP892046-A2.
 PD 20-JAN-1999.
 PA (JCRP-) JCR PHARM CO LTD.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 2; Length 350;
 RESULT 920
 ID ABP81840 standard; protein; 350 AA.
 DE Human melatonin receptor type 1a protein SEQ ID NO:164.
 PN WO200261087-A2.
 PD 08-AUG-2002.
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 6; Length 350;
 RESULT 921
 ID ADO29552 standard; protein; 350 AA.
 DE Human GPCR MTRN1A, SEQ ID NO:654.
 PN WO2004040000-A2.
 PD 13-MAY-2004.
 PA (PRIM-) PRIMAL INC.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 8; Length 350;
 RESULT 922
 ID ASC08362 standard; protein; 350 AA.
 DE Human melatonin receptor type 1A (MTRN1A).
 PN WO2005078455-A1.
 PD 25-AUG-2005.
 PA (FARB) BAYER HEALTHCARE AG.
 Query Match
 Best Local Similarity 6.2%; Score 74; DB 9; Length 350;
 RESULT 923
 ID AAW19220 standard; protein; 364 AA.
 DE Rat growth hormone secretagogue receptor type Ia.
 PN WO9721730-A1.
 PD 19-JUN-1997.

PA (MERI) MERCK & CO INC.
Query Match 6.2%; Score 74; DB 2; Length 364;
Best Local Similarity 19.4%; Pred. No. 22;
RESULT 924
ID ABM73179 standard; protein; 366 AA.
DE Staphylococcus aureus protein #2419.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.2%; Score 74; DB 6; Length 366;
Best Local Similarity 21.8%; Pred. No. 23;
RESULT 925
ID ABB55224 standard; protein; 442 AA.
DE Lactococcus lactis protein yfcd.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.2%; Score 74; DB 5; Length 442;
Best Local Similarity 20.4%; Pred. No. 29;
RESULT 926
ID ADN23927 standard; protein; 485 AA.
DE Bacterial polypeptide #6580.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 74; DB 8; Length 485;
Best Local Similarity 26.2%; Pred. No. 33;
RESULT 927
ID AAY80509 standard; protein; 492 AA.
DE F. lutescens L-lysine:2-oxoglutarate 6-aminotransferase.
PN WO200008170-A1.
PD 17-FEB-2000.
PA (SAOC) MERCIAN CORP.
Query Match 6.2%; Score 74; DB 3; Length 492;
Best Local Similarity 22.5%; Pred. No. 34;
RESULT 928
ID AAG64105 standard; protein; 493 AA.
DE Flavobacterium lutescens L-lysine-6-aminotransferase.
PN WO200148216-A1.
PD 05-JUL-2001.
PA (SAOC) MERCIAN CORP.
Query Match 6.2%; Score 74; DB 4; Length 493;
Best Local Similarity 22.5%; Pred. No. 34;
RESULT 929
ID AAR54067 standard; protein; 1031 AA.
DE Non-A, non-B hepatitis virus gene #6 product.
PN JP06141870-A.
PD 24-MAY-1994.
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
PA (TOFU) TONEN CORP.
Query Match 6.2%; Score 74; DB 2; Length 1031;
Best Local Similarity 26.2%; Pred. No. 95;
RESULT 930
ID AAR98362 standard; protein; 1031 AA.
DE 5'-UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#6).
PN JP07133291-A.
PD 23-MAY-1995.
PA (TOFU) TONEN CORP.
Query Match 6.2%; Score 74; DB 2; Length 1031;
Best Local Similarity 26.2%; Pred. No. 95;
RESULT 931
ID AAG59839 standard; protein; 120 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77442.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 120;
Best Local Similarity 20.3%; Pred. No. 5.5;
RESULT 932
ID AU25578 standard; protein; 192 AA.
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #25.
PN WO200162797-A2.
PD 30-AUG-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 6.2%; Score 73.5; DB 4; Length 192;
Best Local Similarity 26.3%; Pred. No. 11;
RESULT 933
ID ADU08915 standard; protein; 226 AA.
DE Coronavirus membrane protein seqid 38.
PN WO2004096842-A2.
PD 11-NOV-2004.
PA (BCCA-) BC CANCER AGENCY.
Query Match 6.2%; Score 73.5; DB 8; Length 226;
Best Local Similarity 22.2%; Pred. No. 13;
RESULT 934
ID ABU44044 standard; protein; 268 AA.
DE Protein encoded by Prokaryotic essential gene #29571.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 73.5; DB 6; Length 268;
Best Local Similarity 19.6%; Pred. No. 17;
RESULT 935
ID RAG32488 standard; protein; 282 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39200.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 282;
Best Local Similarity 28.1%; Pred. No. 18;
RESULT 936
ID ADF05982 standard; protein; 312 AA.
DE Bacterial polypeptide #2095.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 73.5; DB 7; Length 312;
Best Local Similarity 17.4%; Pred. No. 21;
RESULT 937
ID AAG51386 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65212.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 377;
Best Local Similarity 28.1%; Pred. No. 27;
RESULT 938
ID AAG32487 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39199.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 377;
Best Local Similarity 28.1%; Pred. No. 27;
RESULT 939
ID ABM92289 standard; protein; 400 AA.
DE M. xanthus protein sequence, seq id 11488.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 6.2%; Score 73.5; DB 9; Length 400;
Best Local Similarity 23.3%; Pred. No. 29;
RESULT 940
ID AQ075734 standard; protein; 404 AA.
DE Codon optimised hCMV IE1 encoded exons 2 and 4.
PN WO2004058166-A2.
PD 15-JUL-2004.
PA (VICA-) VICAL INC.
Query Match 6.2%; Score 73.5; DB 8; Length 404;
Best Local Similarity 19.3%; Pred. No. 30;
RESULT 941
ID AAG51385 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65211.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match
Best Local Similarity 6.2%; Score 73.5; DB 3; Length 442;
RESULT 942
ID AAG32486 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39198.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 3; Length 442;
RESULT 943
ID AAG51384 standard; protein; 489 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65210.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 3; Length 489;
RESULT 944
ID AAB86544 standard; protein; 491 AA.
DE Human cytomegalovirus strain AD169 IE1 protein.
PN WO200163286-A2.
PD 30-AUG-2001.
PA (KERN)/ KERN F.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 4; Length 491;
RESULT 945
ID ADP12517 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #127.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 8; Length 491;
RESULT 946
ID ADP12518 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #128.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 8; Length 491;
RESULT 947
ID ADP12513 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #123.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 8; Length 491;
RESULT 948
ID ADP12514 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #124.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 8; Length 491;
RESULT 949
ID ADQ75725 standard; protein; 491 AA.
DE Wild type hCMV IE1.
PN WO2004058166-A2.
PD 15-JUL-2004.
PA (VICA-) VICAL INC.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 8; Length 491;
RESULT 950
ID ABP73574 standard; protein; 574 AA.
DE Candida albicans essential protein SEQ ID NO 7411.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 5; Length 574;
RESULT 951
ID AED26251 standard; protein; 577 AA.
DE Novel human full-length polypeptide 791CIP2B_12, SEQ ID NO:247.
PN US2005221342-A1.
PD 06-OCT-2005.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 9; Length 577;
RESULT 952
ID ADS28278 standard; protein; 637 AA.
DE Bacterial polypeptide #17311.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 8; Length 637;
RESULT 953
ID ABG29128 standard; protein; 682 AA.
DE Novel human diagnostic protein #29119.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 4; Length 682;
RESULT 954
ID ABB61737 standard; protein; 1287 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12003.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 4; Length 1287;
RESULT 955
ID ADS96670 standard; protein; 1287 AA.
DE Drosophila melanogaster protein, SEQ ID 291.
PN WO2004039999-A2.
PD 13-MAY-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 8; Length 1287;
RESULT 956
ID AAR33214 standard; protein; 3033 AA.
DE NANBH virus strain HC-J8 protein.
PN EP532167-A2.
PD 17-MAR-1993.
PA (IMMO) IMMUNO JAPAN INC.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 2; Length 3033;
RESULT 957
ID ABY03151 standard; protein; 7176 AA.
DE Murine hepatitis virus pollab protein, SEQ:9897.
PN WO2004092360-A2.
PD 28-OCT-2004.
PA (CHIR) CHIRON CORP.
Query Match
Best Local Similarity 6.2%; Score 73.5; DB 8; Length 7176;
RESULT 958
ID AAW20571 standard; protein; 114 AA.
DE H. pylori secreted or periplasmic protein 80257.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match
Best Local Similarity 6.1%; Score 73; DB 2; Length 114;
RESULT 959
ID AAU69567 standard; protein; 189 AA.
DE Human G protein-coupled receptor from cDNA Seq-2643.
PN WO200177330-A2.
PD 18-OCT-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.

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Query Match          6.1%; Score 73; DB 5; Length 189;
Best Local Similarity 20.3%; Pred. No. 12;
RESULT 960
ID ADC97146 standard; protein; 199 AA.
DE E. faecium protein sequence SEQ ID 6773.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match          6.1%; Score 73; DB 7; Length 199;
Best Local Similarity 22.6%; Pred. No. 13;
RESULT 961
ID ABP29367 standard; protein; 249 AA.
DE Streptococcus polypeptide SEQ ID NO 7910.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match          6.1%; Score 73; DB 5; Length 249;
Best Local Similarity 24.6%; Pred. No. 17;
RESULT 962
ID AAU87836 standard; protein; 272 AA.
DE T. aureum 7091 elongase TELO1 from plasmid pRAT-4-A1.
PN WO200208401-A2.
PD 31-JAN-2002.
PA (ABBO-) ABBOTT LAB.
Query Match          6.1%; Score 73; DB 5; Length 272;
Best Local Similarity 19.9%; Pred. No. 20;
RESULT 963
ID ADH80191 standard; protein; 272 AA.
DE Fungal 7091 elongase protein seq id 75.
PN US2003163845-A1.
PD 28-AUG-2003.
PA (MUKE/) MUKERJI P.
PA (LEON/) EUN-YEONG LEONARD A.
PA (HUAN/) HUANG Y.
PA (PERE/) PEREIRA S L.
Query Match          6.1%; Score 73; DB 8; Length 272;
Best Local Similarity 19.9%; Pred. No. 20;
RESULT 964
ID ADW12982 standard; protein; 272 AA.
DE Elongase protein #55.
PN US2005009140-A1.
PD 13-JAN-2005.
PA (MUKE/) MUKERJI P.
PA (LEON/) LEONARD A B.
PA (HUAN/) HUANG Y.
PA (PERE/) PEREIRA S L.
Query Match          6.1%; Score 73; DB 9; Length 272;
Best Local Similarity 19.9%; Pred. No. 20;
RESULT 965
ID ABM73154 standard; protein; 290 AA.
DE Staphylococcus aureus protein #2394.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match          6.1%; Score 73; DB 6; Length 290;
Best Local Similarity 23.4%; Pred. No. 22;
RESULT 966
ID ABR47464 standard; protein; 322 AA.
DE Breast cancer associated protein sequence SEQ ID NO:160.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match          6.1%; Score 73; DB 6; Length 322;
Best Local Similarity 20.6%; Pred. No. 25;
RESULT 967
ID ADN61865 standard; protein; 349 AA.
DE Human novel protein NOV42a.
PN US2004043382-A1.
PD 04-MAR-2004.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
PA (SHEN/) SHENOY S G.
Query Match          6.1%; Score 73; DB 8; Length 364;
Best Local Similarity 19.4%; Pred. No. 29;
RESULT 971
ID ADO23026 standard; protein; 364 AA.
DE Mouse novel GPCR GHSR, SEQ ID NO:125.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIN-) PRIMAL INC.
Query Match          6.1%; Score 73; DB 8; Length 364;
Best Local Similarity 19.4%; Pred. No. 29;
RESULT 972
ID AAW77773 standard; protein; 377 AA.
DE Staphylococcus aureus protein of unknown function.
PN EP841394-A2.
PD 13-MAY-1998.
PA (SMIK-) SMITHKLINE BEECHAM CORP.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
Query Match          6.1%; Score 73; DB 2; Length 377;
Best Local Similarity 23.3%; Pred. No. 31;
RESULT 973
ID AAG50065 standard; protein; 415 AA.
Query Match          6.1%; Score 73; DB 8; Length 349;
Best Local Similarity 24.0%; Pred. No. 28;
RESULT 968
ID AAW19613 standard; protein; 364 AA.
DE Rat growth hormone secretagogue receptor type Ia.
PN WO9722004-A1.
PD 19-JUN-1997.
PA (MERI-) MERCK & CO INC.
Query Match          6.1%; Score 73; DB 2; Length 364;
Best Local Similarity 19.4%; Pred. No. 29;
RESULT 969
ID AAY54565 standard; protein; 364 AA.
DE A mouse growth hormone secretagogue receptor.
PN WO200002918-A1.
PD 20-JAN-2000.
PA (MERI-) MERCK & CO INC.
Query Match          6.1%; Score 73; DB 3; Length 364;
Best Local Similarity 19.4%; Pred. No. 29;
RESULT 970
ID AAB97377 standard; protein; 364 AA.
DE Rat growth hormone secretagogue receptor (GHSR) related protein.
PN WO200132705-A1.
PD 10-MAY-2001.
PA (TAKE-) TAKEDA CHEM IND LTD.
Query Match          6.1%; Score 73; DB 4; Length 364;
Best Local Similarity 19.4%; Pred. No. 29;
RESULT 971
ID ADO23026 standard; protein; 364 AA.
DE Mouse novel GPCR GHSR, SEQ ID NO:125.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIN-) PRIMAL INC.
Query Match          6.1%; Score 73; DB 8; Length 364;
Best Local Similarity 19.4%; Pred. No. 29;
RESULT 972
ID AAW77773 standard; protein; 377 AA.
DE Staphylococcus aureus protein of unknown function.
PN EP841394-A2.
PD 13-MAY-1998.
PA (SMIK-) SMITHKLINE BEECHAM CORP.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
Query Match          6.1%; Score 73; DB 2; Length 377;
Best Local Similarity 23.3%; Pred. No. 31;
RESULT 973
ID AAG50065 standard; protein; 415 AA.

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DE Arabidopsis thaliana protein fragment SEQ ID NO: 63404.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 415;
Best Local Similarity 19.8%; Pred. No. 35;
RESULT 974
ID AAG24013 standard; protein; 427 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27528.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 427;
Best Local Similarity 22.0%; Pred. No. 37;
RESULT 975
ID AAG24012 standard; protein; 430 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27527.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 430;
Best Local Similarity 22.0%; Pred. No. 37;
RESULT 976
ID ABU31419 standard; protein; 453 AA.
DE Protein encoded by Prokaryotic essential gene #16946.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 6; Length 453;
Best Local Similarity 26.5%; Pred. No. 40;
RESULT 977
ID AEA16981 standard; protein; 469 AA.
DE Arabidopsis thaliana protein #40.
PN US2005125159-A1.
PD 09-JUN-2005.
PA (STEI/) STEIN J C.
PA (CAOY/) CAO Y.
Query Match 6.1%; Score 73; DB 9; Length 469;
Best Local Similarity 19.8%; Pred. No. 42;
RESULT 978
ID AAG50064 standard; protein; 472 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63403.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 472;
Best Local Similarity 19.8%; Pred. No. 42;
RESULT 979
ID AAG50063 standard; protein; 474 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63402.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 474;
Best Local Similarity 19.8%; Pred. No. 43;
RESULT 980
ID ABW70313 standard; protein; 490 AA.
DE Photobacterium luminescens protein sequence #3410.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.1%; Score 73; DB 6; Length 490;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 981
ID AAY33766 standard; protein; 495 AA.
DE hkv5.1 human brain-specific potassium channel.
PN WO9941372-A1.
PD 19-AUG-1999.
PA (ZENE) ZENECA LTD.
Query Match 6.1%; Score 73; DB 2; Length 495;
Best Local Similarity 23.2%; Pred. No. 45;
RESULT 982
ID ABO63300 standard; protein; 501 AA.
DE Klebsiella pneumoniae polypeptide seqid 9817.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.1%; Score 73; DB 4; Length 748;
Best Local Similarity 23.3%; Pred. No. 80;
Query Match 6.1%; Score 73; DB 7; Length 501;
Best Local Similarity 26.5%; Pred. No. 46;
RESULT 983
ID ABP53583 standard; protein; 526 AA.
DE Human NOVI3b protein SEQ ID NO:30.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 5; Length 526;
Best Local Similarity 23.3%; Pred. No. 49;
RESULT 984
ID ADH42229 standard; protein; 526 AA.
DE Novel human protein NOV50d.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 73; DB 8; Length 526;
Best Local Similarity 23.3%; Pred. No. 49;
RESULT 985
ID ABU31136 standard; protein; 553 AA.
DE Protein encoded by Prokaryotic essential gene #16663.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 6; Length 553;
Best Local Similarity 19.6%; Pred. No. 53;
RESULT 986
ID AAG24011 standard; protein; 556 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27526.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 73; DB 3; Length 556;
Best Local Similarity 22.0%; Pred. No. 53;
RESULT 987
ID ADQ96000 standard; protein; 608 AA.
DE T cell activation associated protein #89.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.1%; Score 73; DB 8; Length 608;
Best Local Similarity 19.5%; Pred. No. 60;
RESULT 988
ID ADR99134 standard; protein; 635 AA.
DE Human protein similar to yeast SSM4, TEB4, SEQ ID 140.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 6.1%; Score 73; DB 8; Length 635;
Best Local Similarity 19.5%; Pred. No. 64;
RESULT 989
ID ABB71311 standard; protein; 717 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40725.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.1%; Score 73; DB 4; Length 717;
Best Local Similarity 21.3%; Pred. No. 76;
RESULT 990
ID AAW26673 standard; protein; 746 AA.
DE Staphylococcus aureus spoIIIE protein.
PN WO9726338-A1.
PD 24-JUL-1997.
PA (SMIX) SMITHKLINE BEECHAM PLC.
Query Match 6.1%; Score 73; DB 2; Length 746;
Best Local Similarity 23.3%; Pred. No. 80;
RESULT 991
ID AAU37199 standard; protein; 748 AA.
DE Staphylococcus aureus cellular proliferation protein #1369.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 4; Length 748;
Best Local Similarity 23.3%; Pred. No. 80;

RESULT 992
ID AAW88407 standard; protein; 750 AA.
DE Human adult neural tissue secreted protein s195_10.
PN WO9857976-A1.
PD 23-DEC-1998.
PA (GEM) GENETICS INST INC.
Query Match 6.1%; Score 73; DB 2; Length 750;
Best Local Similarity 19.5%; Pred. No. 80;
RESULT 993
ID AED72894 standard; protein; 750 AA.
DE Human clone s195_10 encoding cDNA SEQ ID NO:86.
PN US2005250180-A1.
PD 10-NOV-2005.
PA (JACO) JACOBS K.
PA (MCCO) MCCOY J M.
PA (LAVA) LAVALLIE E R.
PA (COLL) COLLINS-RACIE L A.
PA (EVAN) EVANS C.
PA (MERB) MERBERG D.
PA (TREA) TREACY M.
PA (SPAUL) SPAULDING V.
Query Match 6.1%; Score 73; DB 9; Length 750;
Best Local Similarity 19.5%; Pred. No. 80;
RESULT 994
ID AAW26672 standard; protein; 788 AA.
DE Staphylococcus aureus spoIIIE protein.
PN WO9726338-A1.
PD 24-JUL-1997.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.1%; Score 73; DB 2; Length 788;
Best Local Similarity 23.3%; Pred. No. 86;
RESULT 995
ID ABU42392 standard; protein; 788 AA.
DE Protein encoded by Prokaryotic essential gene #27919.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 6; Length 788;
Best Local Similarity 23.3%; Pred. No. 86;
RESULT 996
ID AAU36734 standard; protein; 792 AA.
DE Staphylococcus aureus cellular proliferation protein #904.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 73; DB 4; Length 792;
Best Local Similarity 23.3%; Pred. No. 87;
RESULT 997
ID ABU19057 standard; protein; 792 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 334.
PN WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match 6.1%; Score 73; DB 6; Length 792;
Best Local Similarity 23.3%; Pred. No. 87;
RESULT 998
ID ABM73117 standard; protein; 792 AA.
DE Staphylococcus aureus protein #2357.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.1%; Score 73; DB 6; Length 792;
Best Local Similarity 23.3%; Pred. No. 87;
RESULT 999
ID AAW68466 standard; protein; 845 AA.
DE Protein encoded by fragment #6 isolated from Hepatitis C virus genome.
PN WO9825960-A1.
PD 18-JUN-1998.
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
Query Match 6.1%; Score 73; DB 2; Length 845;
Best Local Similarity 26.2%; Pred. No. 95;
RESULT 1000
ID ADQ95946 standard; protein; 910 AA.
DE T cell activation associated protein #62.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.1%; Score 73; DB 8; Length 910;
Best Local Similarity 19.5%; Pred. No. 1.1e+02;
RESULT 1001
ID ABG24246 standard; protein; 913 AA.
DE Novel human diagnostic protein #24237.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 73; DB 4; Length 913;
Best Local Similarity 19.5%; Pred. No. 1.1e+02;
RESULT 1002
ID AAM51861 standard; protein; 966 AA.
DE Murine polycystic kidney disease protein 2.
PN WO200177331-A1.
PD 18-OCT-2001.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.1%; Score 73; DB 5; Length 966;
Best Local Similarity 21.3%; Pred. No. 1.1e+02;
RESULT 1003
ID ABB07819 standard; protein; 966 AA.
DE Mouse polycystic kidney disease protein 2.
PN US2002035056-A1.
PD 21-MAR-2002.
PA (CURT) CURTIS R A J.
PA (SILO) SILOS-SANTIAGO I.
Query Match 6.1%; Score 73; DB 5; Length 966;
Best Local Similarity 21.3%; Pred. No. 1.1e+02;
RESULT 1004
ID ADJ76159 standard; protein; 966 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1411.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 6.1%; Score 73; DB 8; Length 966;
Best Local Similarity 21.3%; Pred. No. 1.1e+02;
RESULT 1005
ID ADV66235 standard; protein; 966 AA.
DE Polycystic kidney disease protein 2, SEQ ID 11.
PN US2004248160-A1.
PD 09-DEC-2004.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.1%; Score 73; DB 9; Length 966;
Best Local Similarity 21.3%; Pred. No. 1.1e+02;
RESULT 1006
ID ADZ26335 standard; protein; 966 AA.
DE Human hypoxia-responsive protein CNGH0002.1.
PN WO2005033293-A2.
PD 14-APR-2005.
PA (CENZ) CENTOCOR INC.
Query Match 6.1%; Score 73; DB 9; Length 966;
Best Local Similarity 19.5%; Pred. No. 1.1e+02;
RESULT 1007
ID ABG05866 standard; protein; 971 AA.
DE Novel human diagnostic protein #5857.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 73; DB 4; Length 971;
Best Local Similarity 19.5%; Pred. No. 1.1e+02;
RESULT 1008
ID ADR99135 standard; protein; 971 AA.
DE Human protein similar to yeast SSM4, TEB4, SEQ ID 141.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (PARB) BAYER PHARM CORP.
Query Match 6.1%; Score 73; DB 8; Length 971;
Best Local Similarity 19.5%; Pred. No. 1.1e+02;
RESULT 1009
ID ADZ11480 standard; protein; 971 AA.

DE MARCH VI protein, SEQ ID 49.
PN US2005079613-A1.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match 6.1%; Score 73; DB 9; Length 971;
Best Local Similarity 19.5%; Pred. No. 1.1e+02;
RESULT 1010
ID AD211490 standard; protein; 971 AA.
DE MARCH VI protein, SEQ ID 59.
PN US2005079613-A1.
PD 14-APR-2005.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match 6.1%; Score 73; DB 9; Length 971;
Best Local Similarity 19.5%; Pred. No. 1.1e+02;
RESULT 1011
ID ABG07373 standard; protein; 976 AA.
DE Novel human diagnostic protein #7364.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 73; DB 4; Length 976;
Best Local Similarity 19.5%; Pred. No. 1.2e+02;
RESULT 1012
ID ADX40795 standard; protein; 3010 AA.
DE HCV polymerase protein #18.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMUNE INC.
Query Match 6.1%; Score 73; DB 9; Length 3010;
Best Local Similarity 26.2%; Pred. No. 5.5e+02;
RESULT 1013
ID ABU05456 standard; protein; 209 AA.
DE M. tuberculosis and M. leprae marker protein #107.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP-) INST PASTEUR.
Query Match 6.1%; Score 72.5; DB 5; Length 209;
Best Local Similarity 22.1%; Pred. No. 16;
RESULT 1014
ID ABU5302 standard; protein; 222 AA.
DE Protein encoded by Prokaryotic essential gene #829.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 72.5; DB 6; Length 222;
Best Local Similarity 20.5%; Pred. No. 17;
RESULT 1015
ID ADY24595 standard; protein; 274 AA.
DE Plant full length insert polypeptide seqid 72379.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.1%; Score 72.5; DB 8; Length 274;
Best Local Similarity 26.5%; Pred. No. 23;
RESULT 1016
ID ADX95386 standard; protein; 274 AA.
DE Plant full length insert polypeptide seqid 58050.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.1%; Score 72.5; DB 8; Length 274;
Best Local Similarity 26.5%; Pred. No. 23;
RESULT 1017

ID ABB53879 standard; protein; 307 AA.
DE Lactococcus lactis protein yfgg.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 72.5; DB 5; Length 307;
Best Local Similarity 22.9%; Pred. No. 27;
RESULT 1018
ID ADY10668 standard; protein; 307 AA.
DE Plant full length insert polypeptide seqid 66483.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.1%; Score 72.5; DB 8; Length 307;
Best Local Similarity 25.3%; Pred. No. 27;
RESULT 1019
ID ADY11265 standard; protein; 307 AA.
DE Plant full length insert polypeptide seqid 67080.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.1%; Score 72.5; DB 8; Length 307;
Best Local Similarity 25.3%; Pred. No. 27;
RESULT 1020
ID ADY10993 standard; protein; 307 AA.
DE Plant full length insert polypeptide seqid 66808.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.1%; Score 72.5; DB 8; Length 307;
Best Local Similarity 25.3%; Pred. No. 27;
RESULT 1021
ID ADY11014 standard; protein; 308 AA.
DE Plant full length insert polypeptide seqid 66829.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.1%; Score 72.5; DB 8; Length 307;
Best Local Similarity 25.3%; Pred. No. 27;
RESULT 1022
ID ADY10930 standard; protein; 310 AA.
DE Plant full length insert polypeptide seqid 66745.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.1%; Score 72.5; DB 8; Length 308;
Best Local Similarity 25.3%; Pred. No. 27;
RESULT 1023
ID ADY10930 standard; protein; 310 AA.
DE Plant full length insert polypeptide seqid 66745.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.1%; Score 72.5; DB 8; Length 310;
Best Local Similarity 25.3%; Pred. No. 27;

ID ADY11546 standard; protein; 310 AA.
DE Plant full length insert polypeptide seqid 67361.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 310;
Best Local Similarity 25.3%; Pred. No. 27;
RESULT 1024
ID ADY09462 standard; protein; 311 AA.
DE Plant full length insert polypeptide seqid 65277.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 311;
Best Local Similarity 25.3%; Pred. No. 27;
RESULT 1025
ID ADY11115 standard; protein; 312 AA.
DE Plant full length insert polypeptide seqid 66930.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 312;
Best Local Similarity 25.3%; Pred. No. 27;
RESULT 1026
ID ADY10946 standard; protein; 312 AA.
DE Plant full length insert polypeptide seqid 66761.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 312;
Best Local Similarity 25.3%; Pred. No. 27;
RESULT 1027
ID ABB53675 standard; protein; 325 AA.
DE Lactococcus lactis protein ydHB.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 5; Length 325;
Best Local Similarity 25.9%; Pred. No. 29;
RESULT 1028
ID ADH87677 standard; protein; 353 AA.
DE Enterococcus faecalis polypeptide #2157.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 7; Length 353;
Best Local Similarity 21.5%; Pred. No. 32;
RESULT 1029
ID ADH87557 standard; protein; 359 AA.
DE Enterococcus faecalis polypeptide #2037.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 7; Length 359;
Best Local Similarity 21.5%; Pred. No. 32;
RESULT 1030
ID AAR37264 standard; protein; 389 AA.
DE Oxytocin receptor.
PN EP542424-A1.
PD 19-MAY-1993.
PA (ROHT) ROHTO PHARM CO LTD.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 2; Length 389;
Best Local Similarity 24.5%; Pred. No. 37;
RESULT 1031
ID AAW23832 standard; protein; 389 AA.
DE Human oxytocin receptor.
PN EP811684-A2.
PD 10-DEC-1997.
PA (ROHT) ROHTO PHARM CO LTD.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 2; Length 389;
Best Local Similarity 24.5%; Pred. No. 37;
RESULT 1032
ID AAM40217 standard; protein; 389 AA.
DE Human polypeptide SEQ ID NO 3362.
PN WO200153112-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 4; Length 389;
Best Local Similarity 24.5%; Pred. No. 37;
RESULT 1033
ID ABP81865 standard; protein; 389 AA.
DE Human oxytocin receptor protein SEQ ID NO:215.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 6; Length 389;
Best Local Similarity 24.5%; Pred. No. 37;
RESULT 1034
ID AAE38317 standard; protein; 389 AA.
DE Human oxytocin receptor protein.
PN WO2003064402-A1.
PD 07-AUG-2003.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 6; Length 389;
Best Local Similarity 24.5%; Pred. No. 37;
RESULT 1035
ID ADF12125 standard; protein; 389 AA.
DE Human oxytocin receptor (OXTR) protein SEQ ID NO:2.
PN WO2003031816-A2.
PD 13-NOV-2003.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 37;
RESULT 1036
ID ADI03915 standard; protein; 389 AA.
DE Human oxytocin receptor polypeptide.
PN WO2004000993-A2.
PD 31-DEC-2003.
PA (UYQU-) UNIV QUEBEC A MONTREAL.
PA (UYMO-) UNIV MONTREAL CENT HOSPITALIER.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 37;
RESULT 1037
ID ADO29590 standard; protein; 389 AA.
DE Human GPCR OXTR, SEQ ID NO:692.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 37;
RESULT 1038
ID ADW98687 standard; protein; 389 AA.
DE Human oxytocin receptor (OXTR) protein SeqID1.

PN WO2005012565-A1.
PD 10-FEB-2005.
PA (ASTR) ASTRAZENECA AB.
PA (ASTR) ASTRAZENECA UK LTD.
Query Match 6.1%; Score 72.5; DB 9; Length 389;
Best Local Similarity 24.5%; Pred. No. 37;
RESULT 1039
ID AAR58665 standard; protein; 448 AA.
DE Bovine PACAP receptor type 1B mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 448;
Best Local Similarity 29.6%; Pred. No. 45;
RESULT 1040
ID AAR58663 standard; protein; 476 AA.
DE Bovine PACAP receptor type 1A mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 476;
Best Local Similarity 29.6%; Pred. No. 49;
RESULT 1041
ID AAR58657 standard; protein; 485 AA.
DE Bovine PACAP receptor type 1B protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 485;
Best Local Similarity 29.6%; Pred. No. 50;
RESULT 1042
ID AAR58655 standard; protein; 513 AA.
DE Bovine PACAP receptor type 1A protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 513;
Best Local Similarity 29.6%; Pred. No. 54;
RESULT 1043
ID ADN19765 standard; protein; 522 AA.
DE Bacterial polypeptide #2418.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.1%; Score 72.5; DB 8; Length 522;
Best Local Similarity 22.5%; Pred. No. 56;
RESULT 1044
ID ADV89115 standard; protein; 666 AA.
DE Streptococcus agalactiae protein sequence, SEQ ID 1509.
PN FR2824074-A1.
PD 31-OCT-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.1%; Score 72.5; DB 8; Length 666;
Best Local Similarity 23.1%; Pred. No. 78;
RESULT 1045
ID ADV82479 standard; protein; 666 AA.
DE Streptococcus agalactiae protein, SEQ ID 3620.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.1%; Score 72.5; DB 8; Length 666;
Best Local Similarity 23.1%; Pred. No. 78;
RESULT 1046
ID ADV80368 standard; protein; 666 AA.
DE Streptococcus agalactiae protein, SEQ ID 1509.
PN WO200292818-A2.
PD 21-NOV-2002.

PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.1%; Score 72.5; DB 8; Length 666;
Best Local Similarity 23.1%; Pred. No. 78;
RESULT 1047
ID ADI81620 standard; protein; 769 AA.
DE C. elegans protein similar to Pfam PF00023.
PN US2004009537-A1.
PD 15-JAN-2004.
PA (ROOS/) ROOS J.
PA (STAU/) STAUDERMAN K.
PA (VELI/) VELICELEBI G.
Query Match 6.1%; Score 72.5; DB 8; Length 769;
Best Local Similarity 20.2%; Pred. No. 95;
RESULT 1048
ID ABB05429 standard; protein; 848 AA.
DE Arabidopsis thaliana ABH1 protein SEQ ID NO:2.
PN WO200196585-A2.
PD 20-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.1%; Score 72.5; DB 5; Length 848;
Best Local Similarity 22.3%; Pred. No. 1.1e+02;
RESULT 1049
ID AAE31528 standard; protein; 848 AA.
DE Arabidopsis thaliana protein used to isolate rice CBP80 orthologues.
PN WO200281696-A2.
PD 17-OCT-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.1%; Score 72.5; DB 6; Length 848;
Best Local Similarity 22.3%; Pred. No. 1.1e+02;
RESULT 1050
ID ABU25159 standard; protein; 851 AA.
DE Protein encoded by Prokaryotic essential gene #10686.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 72.5; DB 6; Length 851;
Best Local Similarity 20.5%; Pred. No. 1.1e+02;
RESULT 1051
ID ADY10144 standard; protein; 903 AA.
DE Plant full length insert polypeptide seqid 65959.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match 6.1%; Score 72.5; DB 8; Length 903;
Best Local Similarity 18.1%; Pred. No. 1.2e+02;
RESULT 1052
ID ADW76078 standard; protein; 1051 AA.
DE Human cytomegalovirus (HCMV) pp65-IE1 fusion protein.
PN WO2005007689-A1.
PD 27-JAN-2005.
PA (ALPH-) ALPHAVAX INC.
Query Match 6.1%; Score 72.5; DB 9; Length 1051;
Best Local Similarity 19.3%; Pred. No. 1.5e+02;
RESULT 1053
ID AAR34580 standard; protein; 3010 AA.
DE Human hepatitis C virus gene encoded polypeptide.
PN EP541089-A2.
PD 12-MAY-1993.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
Query Match 6.1%; Score 72.5; DB 2; Length 3010;
Best Local Similarity 23.7%; Pred. No. 6.3e+02;
RESULT 1054
ID ADQ96378 standard; protein; 208 AA.
DE T cell activation associated protein #278.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASahi KASEI PHARMA CORP.

Query Match 6.0%; Score 72; DB 8; Length 208;
Best Local Similarity 20.8%; Pred. No. 18;
RESULT 1055
ID AED36113 standard; protein; 260 AA.
DE Tobacco NAPI-like protein (NENAP1b).
PN WO2005094562-A1.
PD 13-OCT-2005.
PA (CROP-) CROPDESIGN NV.
Query Match 6.0%; Score 72; DB 9; Length 260;
Best Local Similarity 31.6%; Pred. No. 24;
RESULT 1056
ID ABB48543 standard; protein; 306 AA.
DE Listeria monocytogenes protein #1247.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.0%; Score 72; DB 5; Length 306;
Best Local Similarity 21.0%; Pred. No. 30;
RESULT 1057
ID ABU39432 standard; protein; 317 AA.
DE Protein encoded by Prokaryotic essential gene #24959.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 317;
Best Local Similarity 23.5%; Pred. No. 32;
RESULT 1058
ID AAB53392 standard; protein; 334 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:932.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 72; DB 3; Length 334;
Best Local Similarity 28.8%; Pred. No. 34;
RESULT 1059
ID AAY87505 standard; protein; 370 AA.
DE Human G coupled-protein receptor, hGR3.
PN WO200017641-A1.
PD 30-MAR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 370;
Best Local Similarity 21.8%; Pred. No. 40;
RESULT 1060
ID AAW20731 standard; protein; 375 AA.
DE H. pylori inner membrane protein, O6cp1118orf6.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.0%; Score 72; DB 2; Length 375;
Best Local Similarity 20.9%; Pred. No. 40;
RESULT 1061
ID ABU19932 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #5459.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 396;
Best Local Similarity 21.6%; Pred. No. 43;
RESULT 1062
ID ABG25051 standard; protein; 414 AA.
DE Novel human diagnostic protein #25042.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 72; DB 4; Length 414;
Best Local Similarity 22.6%; Pred. No. 46;
RESULT 1063
ID AAG50203 standard; protein; 427 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63592.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 427;
Best Local Similarity 22.0%; Pred. No. 48;

RESULT 1064
ID AAG50202 standard; protein; 430 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63591.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 430;
Best Local Similarity 22.0%; Pred. No. 49;
RESULT 1065
ID ABM72825 standard; protein; 447 AA.
DE Staphylococcus aureus protein #2065.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.0%; Score 72; DB 6; Length 447;
Best Local Similarity 23.9%; Pred. No. 51;
RESULT 1066
ID ABB62902 standard; protein; 448 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15498.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 72; DB 4; Length 448;
Best Local Similarity 25.1%; Pred. No. 52;
RESULT 1067
ID ABJ18913 standard; protein; 453 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 59.
PN WO200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match 6.0%; Score 72; DB 6; Length 453;
Best Local Similarity 23.9%; Pred. No. 52;
RESULT 1068
ID ABU16441 standard; protein; 453 AA.
DE Protein encoded by Prokaryotic essential gene #1969.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 453;
Best Local Similarity 23.9%; Pred. No. 52;
RESULT 1069
ID ADN73057 standard; protein; 468 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 952.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 6.0%; Score 72; DB 8; Length 468;
Best Local Similarity 21.8%; Pred. No. 55;
RESULT 1070
ID AAG16338 standard; protein; 495 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16945.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 495;
Best Local Similarity 21.3%; Pred. No. 59;
RESULT 1071
ID AAG16337 standard; protein; 497 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16944.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 497;
Best Local Similarity 21.3%; Pred. No. 60;
RESULT 1072
ID AED61108 standard; protein; 497 AA.
DE Thale cress protein #81.
PN US2005246785-A1.
PD 03-NOV-2005.
PA (CERE-) CERES INC.
Query Match 6.0%; Score 72; DB 9; Length 497;
Best Local Similarity 21.3%; Pred. No. 60;
RESULT 1073
ID AEF26566 standard; protein; 497 AA.
DE A. thaliana cytochrome P450 homolog SEQ ID NO: 85.
PN US2006015970-A1.

PD 19-JAN-2006.
 PA (CERS-) CERS INC.
 Query Match 6.0%; Score 72; DB 10; Length 497;
 Best Local Similarity 21.3%; Pred. No. 60;
 RESULT 1074
 ID AGI6336 standard; protein; 507 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 16943.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 6.0%; Score 72; DB 3; Length 507;
 Best Local Similarity 21.3%; Pred. No. 61;
 RESULT 1075
 ID ADS3568 standard; protein; 543 AA.
 DE Bacterial polypeptide #12601.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 6.0%; Score 72; DB 8; Length 543;
 Best Local Similarity 18.6%; Pred. No. 67;
 RESULT 1076
 ID ABU25738 standard; protein; 552 AA.
 DE Protein encoded by Prokaryotic essential gene #11265.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.0%; Score 72; DB 6; Length 552;
 Best Local Similarity 19.5%; Pred. No. 69;
 RESULT 1077
 ID AAG50201 standard; protein; 556 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63590.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match 6.0%; Score 72; DB 3; Length 556;
 Best Local Similarity 22.0%; Pred. No. 70;
 RESULT 1078
 ID ADJ69383 standard; protein; 594 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID1189.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 6.0%; Score 72; DB 7; Length 594;
 Best Local Similarity 20.8%; Pred. No. 76;
 RESULT 1079
 ID ABP97202 standard; protein; 696 AA.
 DE Tumour-associated antigenic target protein TAT247 SEQ ID NO:84.
 PN WO2003024392-A2.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.0%; Score 72; DB 6; Length 696;
 Best Local Similarity 20.8%; Pred. No. 95;
 RESULT 1080
 ID ABP97201 standard; protein; 696 AA.
 DE Tumour-associated antigenic target protein TAT225 SEQ ID NO:83.
 PN WO2003024392-A2.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.0%; Score 72; DB 6; Length 696;
 Best Local Similarity 20.8%; Pred. No. 95;
 RESULT 1081
 ID ABP81969 standard; protein; 696 AA.
 DE Human GPCR XPR1 protein SEQ ID NO:424.
 PN WO200261087-A2.
 PD 08-AUG-2002.
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 Query Match 6.0%; Score 72; DB 6; Length 696;
 Best Local Similarity 20.8%; Pred. No. 95;
 RESULT 1082
 ID ADB67652 standard; protein; 696 AA.

DE Human xenotropic polytropic retrovirus receptor, SEQ ID 21.
 PN WO2003072824-A1.
 PD 04-SEP-2003.
 PA (SANY) SANKYO CO LTD.
 Query Match 6.0%; Score 72; DB 7; Length 696;
 Best Local Similarity 20.8%; Pred. No. 95;
 RESULT 1083
 ID ADQ96380 standard; protein; 696 AA.
 DE T cell activation associated protein #279.
 PN WO2004058805-A2.
 PD 15-JUL-2004.
 PA (ASAH-) ASahi KASEI PHARMA CORP.
 Query Match 6.0%; Score 72; DB 8; Length 696;
 Best Local Similarity 20.8%; Pred. No. 95;
 RESULT 1084
 ID ABM69179 standard; protein; 724 AA.
 DE Photorehabdus luminescens protein sequence #2276.
 PN WO200294867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 6.0%; Score 72; DB 6; Length 724;
 Best Local Similarity 21.3%; Pred. No. 1e+02;
 RESULT 1085
 ID AAB46702 standard; protein; 741 AA.
 DE P. falciparum DNA polymerase protein fragment SEQ ID NO 11.
 PN WO200075335-A2.
 PD 14-DEC-2000.
 PA (DECO-) DECODE GENETICS EHP.
 Query Match 6.0%; Score 72; DB 4; Length 741;
 Best Local Similarity 30.4%; Pred. No. 1e+02;
 RESULT 1086
 ID AAM47977 standard; protein; 788 AA.
 DE Human HARRG.
 PN CN1315342-A.
 PD 03-OCT-2001.
 PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
 Query Match 6.0%; Score 72; DB 5; Length 788;
 Best Local Similarity 26.3%; Pred. No. 1.1e+02;
 RESULT 1087
 ID ABB58917 standard; protein; 1275 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 3543.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 6.0%; Score 72; DB 4; Length 1275;
 Best Local Similarity 19.0%; Pred. No. 2.2e+02;
 RESULT 1088
 ID AAY70064 standard; protein; 2307 AA.
 DE Recombinant fusion pHCAP-1 polypeptide.
 PN WO200008469-A1.
 PD 17-FEB-2000.
 PA (AGOU-) AGOURON PHARM INC.
 Query Match 6.0%; Score 72; DB 3; Length 2307;
 Best Local Similarity 23.6%; Pred. No. 5e+02;
 RESULT 1089
 ID AAY70065 standard; protein; 2307 AA.
 DE Recombinant fusion pHCAP-3 polypeptide.
 PN WO200008469-A1.
 PD 17-FEB-2000.
 PA (AGOU-) AGOURON PHARM INC.
 Query Match 6.0%; Score 72; DB 3; Length 2307;
 Best Local Similarity 23.6%; Pred. No. 5e+02;
 RESULT 1090
 ID AAY70066 standard; protein; 2307 AA.
 DE Recombinant fusion pHCAP-4 polypeptide.
 PN WO200008469-A1.
 PD 17-FEB-2000.
 PA (AGOU-) AGOURON PHARM INC.
 Query Match 6.0%; Score 72; DB 3; Length 2307;
 Best Local Similarity 23.6%; Pred. No. 5e+02;
 RESULT 1091
 ID AAM93791 standard; protein; 208 AA.

DE Human polypeptide, SEQ ID NO: 3817.
PN EPI130094-A2.
PA (HELI-) HELIX RES INST.
Query Match 6.0%; Score 71.5; DB 4; Length 208;
Best Local Similarity 25.2%; Pred. No. 20;
RESULT 1092
ID ADL31784 standard; protein; 208 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3817.
PN EPI1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIO TECHNOLOGY.
Query Match 6.0%; Score 71.5; DB 8; Length 208;
Best Local Similarity 25.2%; Pred. No. 20;
RESULT 1093
ID AAG56417 standard; protein; 209 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 72517.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 71.5; DB 3; Length 209;
Best Local Similarity 25.6%; Pred. No. 21;
RESULT 1094
ID AAG56416 standard; protein; 216 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 72516.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 71.5; DB 3; Length 216;
Best Local Similarity 25.6%; Pred. No. 21;
RESULT 1095
ID AAG16922 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17750.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 71.5; DB 3; Length 218;
Best Local Similarity 42.4%; Pred. No. 22;
RESULT 1096
ID ABB53486 standard; protein; 301 AA.
DE Lactococcus lactis protein ybiG.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.0%; Score 71.5; DB 5; Length 301;
Best Local Similarity 26.5%; Pred. No. 34;
RESULT 1097
ID AAW37976 standard; protein; 342 AA.
DE Kaposi's sarcoma associated herpesvirus G protein-coupled receptor.
PN W09815289-A1.
PD 16-APR-1998.
PA (CORR) CORNELL RES FOUND INC.
Query Match 6.0%; Score 71.5; DB 2; Length 342;
Best Local Similarity 22.2%; Pred. No. 41;
RESULT 1098
ID ADG87423 standard; protein; 348 AA.
DE Meloidogyne incognita plk1 protein.
PN US2003150017-A1.
PD 07-AUG-2003.
PA (MESA/) MESA J R B.
PA (GRAH/) GRAHAM M W.
PA (FAIR/) FAIRBAIRN D J.
Query Match 6.0%; Score 71.5; DB 7; Length 348;
Best Local Similarity 21.0%; Pred. No. 42;
RESULT 1099
ID AEF77681 standard; protein; 362 AA.
DE Rat prostaglandin E receptor 2 (PTGER2).
PN W02060171-A2.
PD 16-FEB-2006.
PA (META-) METABOLEX INC.
Query Match 6.0%; Score 71.5; DB 10; Length 362;
Best Local Similarity 24.2%; Pred. No. 44;
RESULT 1100
ID ADR40542 standard; protein; 363 AA.
DE Ovine MLJA protein.
PN US2004161823-A1.

PD 19-AUG-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
PA (HAWK/) HAWKEN D R.
Query Match 6.0%; Score 71.5; DB 8; Length 363;
Best Local Similarity 23.1%; Pred. No. 44;
RESULT 1101
ID AAR88410 standard; protein; 366 AA.
DE High-affinity melatonin-1a receptor.
PN W0953320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 6.0%; Score 71.5; DB 2; Length 366;
Best Local Similarity 23.1%; Pred. No. 45;
RESULT 1102
ID ABU03456 standard; protein; 382 AA.
DE Angiogenesis-associated human protein sequence #1.
PN W0200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.0%; Score 71.5; DB 6; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1103
ID ABP58069 standard; protein; 382 AA.
DE Human G-protein coupled receptor GAVEL.
PN W0200295056-A2.
PD 28-NOV-2002.
PA (AVET) AVENTIS PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1104
ID ABP59277 standard; protein; 382 AA.
DE Human Edg1 receptor.
PN W02003006503-A1.
PD 23-JAN-2003.
PA (CERE-) CERETEK.
Query Match 6.0%; Score 71.5; DB 6; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1105
ID ABU08809 standard; protein; 382 AA.
DE Human EDG-1 protein.
PN US2002155512-A1.
PD 24-OCT-2002.
PA (RIGE-) RIGEL PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1106
ID ABR59701 standard; protein; 382 AA.
DE Human endothelial differentiation sphingolipid GPCR 1.
PN W02003029277-A2.
PD 10-APR-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1107
ID ABP81876 standard; protein; 382 AA.
DE Human sphingolipid receptor Edg1 protein SEQ ID NO:237.
PN W0200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.0%; Score 71.5; DB 6; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1108
ID ADB67662 standard; protein; 382 AA.
DE Human EDG1, SEQ ID 31.
PN W02003072824-A1.
PD 04-SEP-2003.
PA (SANY) SANKYO CO LTD.
Query Match 6.0%; Score 71.5; DB 7; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1109
ID ADC40477 standard; protein; 382 AA.

DE Protein of human EDG-1.
PN WO2003052096-A1.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.0%; Score 71.5; DB 7; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1110
ID ADN38684 standard; protein; 382 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:2.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.0%; Score 71.5; DB 7; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1111
ID AM85457 standard; protein; 382 AA.
DE Human protein sequence hCPI630135.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 6.0%; Score 71.5; DB 7; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1112
ID ADJ45541 standard; protein; 382 AA.
DE LXR-ligand induced transcript seq id 72.
PN US2004023276-A1.
PD 05-FEB-2004.
PA (WARD/) WARD T R.
PA (MAOM/) MAO M.
PA (LINS/) LINSLEY P S.
PA (LUND/) LUND E.
Query Match 6.0%; Score 71.5; DB 8; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1113
ID ADK67022 standard; protein; 382 AA.
DE Human cancer associated protein sequence SEQ ID NO:68.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.0%; Score 71.5; DB 8; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1114
ID ADY19566 standard; protein; 382 AA.
DE PRO polypeptide SEQ ID NO 5372.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 6.0%; Score 71.5; DB 9; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1115
ID ADZ12973 standard; protein; 382 AA.
DE Human cancer-associated protein #147.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 6.0%; Score 71.5; DB 9; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1116
ID ADZ12973 standard; protein; 382 AA.
DE Human cancer-associated protein #146.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 6.0%; Score 71.5; DB 9; Length 382;
Best Local Similarity 22.3%; Pred. No. 47;
RESULT 1117
ID ADN19614 standard; protein; 383 AA.
DE Bacterial polypeptide #2267.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.0%; Score 71.5; DB 8; Length 383;
Best Local Similarity 22.0%; Pred. No. 48;
RESULT 1118
ID ABB05226 standard; protein; 390 AA.
DE Catostomus commersoni isotocin receptor protein SEQ ID NO:3.
PN WO200192296-A2.
PD 06-DEC-2001.
PA (FARB) BAYER AG.
Query Match 6.0%; Score 71.5; DB 5; Length 390;
Best Local Similarity 22.2%; Pred. No. 49;
RESULT 1119
ID ADM83141 standard; protein; 394 AA.
DE Rat vesicle membrane protein (VMP)2.
PN US2003175787-A1.
PD 18-SEP-2003.
PA (INCY-) INCYTE CORP.
Query Match 6.0%; Score 71.5; DB 7; Length 394;
Best Local Similarity 22.7%; Pred. No. 49;
RESULT 1120
ID ABB48023 standard; protein; 435 AA.
DE Listeria monocytogenes protein #727.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.0%; Score 71.5; DB 5; Length 435;
Best Local Similarity 21.4%; Pred. No. 57;
RESULT 1121
ID AAR22000 standard; protein; 441 AA.
DE Partial M17 antigen from Region II, encoded by PCR prod.
PN WO9203457-A.
PD 05-MAR-1992.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.0%; Score 71.5; DB 2; Length 441;
Best Local Similarity 22.6%; Pred. No. 58;
RESULT 1122
ID ADX93096 standard; protein; 448 AA.
DE Plant full length insert polypeptide seqid 55760.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match 6.0%; Score 71.5; DB 8; Length 448;
Best Local Similarity 22.3%; Pred. No. 59;
RESULT 1123
ID ABP75877 standard; protein; 470 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1061.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 6; Length 470;
Best Local Similarity 22.4%; Pred. No. 63;
RESULT 1124
ID ABU26033 standard; protein; 524 AA.
DE Protein encoded by Prokaryotic essential gene #11560.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 524;
Best Local Similarity 26.6%; Pred. No. 73;
RESULT 1125
ID ABJ37074 standard; protein; 565 AA.
DE Human breast cancer / ovarian cancer related protein #50.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 565;
Best Local Similarity 22.4%; Pred. No. 81;

RESULT 1126
ID AAW51244 standard; protein; 568 AA.
DE Human calcitonin receptor.
PN WO9821242-A1.
PD 22-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 71.5; DB 2; Length 568;
Best Local Similarity 22.4%; Pred. No. 82;
RESULT 1127
ID ABU16392 standard; protein; 603 AA.
DE Protein encoded by Prokaryotic essential gene #1919.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 603;
Best Local Similarity 21.3%; Pred. No. 89;
RESULT 1128
ID ABM72619 standard; protein; 603 AA.
DE Staphylococcus aureus protein #1859.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.0%; Score 71.5; DB 6; Length 603;
Best Local Similarity 21.3%; Pred. No. 89;
RESULT 1129
ID AEC46140 standard; protein; 689 AA.
DE Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 48.
PN US2005191701-A1.
PD 01-SEP-2005.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 9; Length 689;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1130
ID ADM43215 standard; protein; 697 AA.
DE Human methionine synthase reductase del Arg 559 variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 697;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1131
ID ADM43217 standard; protein; 697 AA.
DE Human methionine synthase reductase del Leu 576 variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 697;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1132
ID AEC46138 standard; protein; 697 AA.
DE Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 46.
PN US2005191701-A1.
PD 01-SEP-2005.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 697;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1133
ID AEC46133 standard; protein; 698 AA.
DE Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 44.
PN US2005191701-A1.
PD 01-SEP-2005.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 9; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1134
ID AEC46113 standard; protein; 698 AA.
DE Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 44.
PN US2005191701-A1.
PD 01-SEP-2005.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 9; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1135
ID ADM43211 standard; protein; 698 AA.
DE Human methionine synthase reductase Met221le variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1136
ID ADM43213 standard; protein; 698 AA.
DE Human methionine synthase reductase Cys37Tyr variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1137
ID ADM43207 standard; protein; 698 AA.
DE Human wild-type methionine synthase reductase.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1138
ID ADQ39857 standard; protein; 698 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1520.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 71.5; DB 8; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1139
ID ASC46136 standard; protein; 698 AA.
DE Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 44.
PN US2005191701-A1.
PD 01-SEP-2005.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 9; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1140
ID AEC46113 standard; protein; 698 AA.

ID AAB07591 standard; protein; 698 AA.
DE A human methionine synthase reductase polypeptide.
PN WO200042196-A2.
PD 20-JUL-2000.
PA (UYMC-) UNIV MCGILL.
Query Match 6.0%; Score 71.5; DB 3; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1134
ID ABG00883 standard; protein; 698 AA.
DE Novel human diagnostic protein #874.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 71.5; DB 4; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1135
ID ADM43211 standard; protein; 698 AA.
DE Human methionine synthase reductase Met221le variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1136
ID ADM43213 standard; protein; 698 AA.
DE Human methionine synthase reductase Cys37Tyr variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1137
ID ADM43207 standard; protein; 698 AA.
DE Human wild-type methionine synthase reductase.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1138
ID ADQ39857 standard; protein; 698 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1520.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 71.5; DB 8; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1139
ID ASC46136 standard; protein; 698 AA.
DE Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 44.
PN US2005191701-A1.
PD 01-SEP-2005.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 9; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1140
ID AEC46113 standard; protein; 698 AA.

DE Human methionine synthase reductase (MTRR) protein, SEQ ID NO: 21.
PN US2005191701-A1.
PD 01-SEP-2005.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 9; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1141
ID AEC46134 standard; protein; 698 AA.
DE Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 42.
PN US2005191701-A1.
PD 01-SEP-2005.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 9; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1142
ID AEC46094 standard; protein; 698 AA.
DE Human methionine synthase reductase (MTRR) protein, SEQ ID NO: 2.
PN US2005191701-A1.
PD 01-SEP-2005.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 9; Length 698;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1143
ID ADQ39858 standard; protein; 725 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1521.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 71.5; DB 8; Length 725;
Best Local Similarity 22.8%; Pred. No. 1.2e+02;
RESULT 1144
ID ADU06586 standard; protein; 725 AA.
DE Novel bronchial cancer-associated human protein SeqID812.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 6.0%; Score 71.5; DB 8; Length 725;
Best Local Similarity 22.8%; Pred. No. 1.2e+02;
RESULT 1145
ID AAY51606 standard; protein; 890 AA.
DE Human wml protein.
PN DE19845277-C1.
PD 09-MAR-2000.
PA (UYMU-) UNIV MUEENCHEN MAXIMILIANS LUDWIG.
Query Match 6.0%; Score 71.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.5e+02;
RESULT 1146
ID ABB78282 standard; protein; 890 AA.
DE Amino acid sequence of human wolframin polypeptide.
PN WO200263307-A2.
PD 15-AUG-2002.
PA (PHAA-) PHARMACIA & UPJOHN CO.
Query Match 6.0%; Score 71.5; DB 5; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.5e+02;
RESULT 1147
ID ADD46013 standard; protein; 890 AA.
DE Human Protein O76024, SEQ ID NO 11685.
PN WO2003016475-A2.
PD 27-FEB-2003.

PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 6.0%; Score 71.5; DB 7; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.5e+02;
RESULT 1148
ID ADF69127 standard; protein; 890 AA.
DE Human MP53 protein sequence SEQ ID NO:97.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 6.0%; Score 71.5; DB 7; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.5e+02;
RESULT 1149
ID ADY70426 standard; protein; 890 AA.
DE Human beta-amyloid precursor protein, wolframin.
PN WO2005023858-A1.
PD 17-MAR-2005.
PA (CELL-) CELLZOME AG.
Query Match 6.0%; Score 71.5; DB 9; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.5e+02;
RESULT 1150
ID ADY70680 standard; protein; 890 AA.
DE Human nicastrin/psen2-complex member, wolframin protein.
PN WO2005023833-A2.
PD 17-MAR-2005.
PA (CELL-) CELLZOME AG.
Query Match 6.0%; Score 71.5; DB 9; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.5e+02;
RESULT 1151
ID AEE39892 standard; protein; 890 AA.
DE Amino acid sequence SEQ ID NO:24.
PN WO2005112978-A2.
PD 01-DEC-2005.
PA (UTAH-) UNIV UTAH RES FOUND.
Query Match 6.0%; Score 71.5; DB 10; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.5e+02;
RESULT 1152
ID ADL22689 standard; protein; 2245 AA.
DE Human disease detection and treatment (MDDT) protein - SEQ ID 138.
PN WO2003062379-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 7; Length 2245;
Best Local Similarity 22.4%; Pred. No. 5.5e+02;
RESULT 1153
ID AAB42192 standard; protein; 2405 AA.
DE Human ORFX ORF1956 polypeptide sequence SEQ ID NO:3912.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.0%; Score 71.5; DB 3; Length 2405;
Best Local Similarity 22.4%; Pred. No. 6.1e+02;
RESULT 1154
ID ABB11404 standard; peptide; 2560 AA.
DE Human FLAMINGO 1 homologue, SEQ ID NO:1774.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 71.5; DB 4; Length 2560;
Best Local Similarity 22.4%; Pred. No. 6.6e+02;
RESULT 1155
ID ABU11556 standard; protein; 2894 AA.
DE Human MDDT polypeptide SEQ ID 503.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 6; Length 2894;
Best Local Similarity 22.4%; Pred. No. 7.9e+02;
RESULT 1156
ID AAU07054 standard; protein; 2923 AA.
DE Human Flamingo protein encoded by cDNA splice variant.
PN WO200161003-A1.
PD 23-AUG-2001.

PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.0%; Score 71.5; DB 4; Length 2923;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1157
ID AAM50866 standard; protein; 2923 AA.
DE Cadherin EGF LAG seven-pass G-type receptor 2, basal cell marker.
PN WO200208765-A2.
PD 31-JAN-2002.
PA (STRD) UNIV STANFORD.
PA (GENO-) APPLIED GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 5; Length 2923;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1158
ID ABP82018 standard; protein; 2923 AA.
DE Human GPCR CELSR2 protein SEQ ID NO:524.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIPESPAN BIOSCIENCES INC.
Query Match 6.0%; Score 71.5; DB 6; Length 2923;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1159
ID ADC15499 standard; protein; 2923 AA.
DE Human cadherin EGF LAG seven-pass G-type receptor 2.
PN US2003086934-A1.
PD 08-MAY-2003.
PA (BOTS/) BOTSTEIN D.
PA (BROW/) BROWN P O.
PA (PERO/) PEROU C M.
PA (RING/) RING B.
PA (ROSS/) ROSS D.
PA (SEIT/) SEITZ R.
PA (VRIU/) VAN DE RIJN J M.
Query Match 6.0%; Score 71.5; DB 7; Length 2923;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1160
ID ADC86479 standard; protein; 2923 AA.
DE Human GPCR protein SEQ ID NO:932.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 6.0%; Score 71.5; DB 7; Length 2923;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1161
ID ADE54407 standard; protein; 2923 AA.
DE Human Protein XP_042739, SEQ ID NO 210.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.0%; Score 71.5; DB 7; Length 2923;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1162
ID ADE54411 standard; protein; 2923 AA.
DE Human Protein XP_042739, SEQ ID NO 214.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.0%; Score 71.5; DB 7; Length 2923;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1163
ID ADO29245 standard; protein; 2923 AA.
DE Human GPCR CELSR2, SEQ ID NO:346.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.0%; Score 71.5; DB 8; Length 2923;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1164
ID ADY70314 standard; protein; 2923 AA.
DE Human beta-APP, cadherin EGF LAG seven-pass G-type receptor 2.
PN WO2005023858-A1.

PD 17-MAR-2005.
PA (CELL-) CELLZOME AG.
Query Match 6.0%; Score 71.5; DB 9; Length 2923;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1165
ID ADY70652 standard; protein; 2923 AA.
DE Human BACE1/PTK7-complex member, CELSR2 protein.
PN WO2005023833-A2.
PD 17-MAR-2005.
PA (CELL-) CELLZOME AG.
Query Match 6.0%; Score 71.5; DB 9; Length 2923;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1166
ID ADY70648 standard; protein; 2923 AA.
DE Human BACE1-complex, cadherin seven-pass G-type receptor 2 protein.
PN WO2005023833-A2.
PD 17-MAR-2005.
PA (CELL-) CELLZOME AG.
Query Match 6.0%; Score 71.5; DB 9; Length 2923;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1167
ID AAU74826 standard; protein; 2936 AA.
DE Human REPTR 9 protein.
PN WO200198354-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 5; Length 2936;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1168
ID AAU07053 standard; protein; 2956 AA.
DE Human Flamingo polypeptide.
PN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.0%; Score 71.5; DB 4; Length 2956;
Best Local Similarity 22.4%; Pred. No. 8.1e+02;
RESULT 1169
ID ADX40788 standard; protein; 3010 AA.
DE HCV polymerase protein #11.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMUNE INC.
Query Match 6.0%; Score 71.5; DB 9; Length 3010;
Best Local Similarity 23.7%; Pred. No. 8.3e+02;
RESULT 1170
ID AAR34468 standard; protein; 3011 AA.
DE Encoded by full-length Hepatitis C virus clone JKI-B.
PN JP05068562-A.
PD 23-MAR-1993.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
Query Match 6.0%; Score 71.5; DB 2; Length 3011;
Best Local Similarity 23.7%; Pred. No. 8.3e+02;
RESULT 1171
ID AAR31621 standard; protein; 3011 AA.
DE Hepatitis C virus (HCV) polypeptide.
PN WO9300365-A2.
PD 07-JAN-1993.
PA (CHIR) CHIRON CORP.
Query Match 6.0%; Score 71.5; DB 2; Length 3011;
Best Local Similarity 22.8%; Pred. No. 8.3e+02;
RESULT 1172
ID ABB67866 standard; protein; 5303 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30390.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.0%; Score 71.5; DB 4; Length 5303;
Best Local Similarity 29.5%; Pred. No. 1.8e+03;
RESULT 1173
ID AEF50785 standard; protein; 195 AA.
DE MmMSC A8 clone, hypothetical transmembrane protein #1.
PN WO2006005943-A1.
PD 19-JAN-2006.

PA (MORE-) MOREDUN RES INST.
 Query Match 5.9%; Score 71; DB 10; Length 195;
 Best Local Similarity 25.0%; Pred. No. 21;
 RESULT 1174
 ID ABB06793 standard; protein; 198 AA.
 DE Human transmembrane 4 protein 22 SEQ ID NO:2.
 PN CNI327990-A.
 PD 26-DEC-2001.
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 Query Match 5.9%; Score 71; DB 5; Length 198;
 Best Local Similarity 24.5%; Pred. No. 22;
 RESULT 1175
 ID AEC21170 standard; protein; 217 AA.
 DE L. acidophilus metal-dependent membrane protease #6.
 PN WO2005081959-A2.
 PD 09-SEP-2005.
 PA (UYN-) UNIV NORTH CAROLINA STATE.
 Query Match 5.9%; Score 71; DB 9; Length 217;
 Best Local Similarity 22.4%; Pred. No. 25;
 RESULT 1176
 ID ADU08919 standard; protein; 223 AA.
 DE Coronavirus membrane protein seqid 42.
 PN WO2004096842-A2.
 PD 11-NOV-2004.
 PA (BCCA-) BC CANCER AGENCY.
 Query Match 5.9%; Score 71; DB 8; Length 223;
 Best Local Similarity 22.4%; Pred. No. 26;
 RESULT 1177
 ID ABR58398 standard; protein; 240 AA.
 DE Human NOV17a.
 PN WO2003029423-A2.
 PD 10-APR-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.9%; Score 71; DB 6; Length 240;
 Best Local Similarity 18.6%; Pred. No. 28;
 RESULT 1178
 ID ABP26255 standard; protein; 295 AA.
 DE Streptococcus polypeptide SEQ ID NO 1686.
 PN WO200234771-A2.
 PD 02-MAY-2002.
 PA (CHIR-) CHIRON SPA.
 Query Match 5.9%; Score 71; DB 5; Length 295;
 Best Local Similarity 24.9%; Pred. No. 38;
 RESULT 1179
 ID ADX65958 standard; protein; 309 AA.
 DE Plant full length insert polypeptide seqid 36801.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Query Match 5.9%; Score 71; DB 8; Length 309;
 Best Local Similarity 18.7%; Pred. No. 40;
 RESULT 1180
 ID AAG72952 standard; protein; 310 AA.
 DE Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634.
 PN WO200127158-A2.
 PD 19-APR-2001.
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 Query Match 5.9%; Score 71; DB 4; Length 310;
 Best Local Similarity 22.9%; Pred. No. 41;
 RESULT 1181
 ID AAR48717 standard; protein; 312 AA.
 DE G-protein coupled human interleukin-8 receptor protein.
 PN W09405695-A1.
 PD 17-MAR-1994.
 PA (UYN-) UNIV NEW YORK STATE.
 Query Match 5.9%; Score 71; DB 2; Length 312;

Best Local Similarity 19.7%; Pred. No. 41;
 RESULT 1182
 ID AAW02689 standard; peptide; 312 AA.
 DE G-protein coupled human interleukin-8 receptor.
 PN US5508384-A.
 PD 16-APR-1996.
 PA (UYN-) UNIV NEW YORK STATE.
 Query Match 5.9%; Score 71; DB 2; Length 312;
 Best Local Similarity 19.7%; Pred. No. 41;
 RESULT 1183
 ID AAG72169 standard; protein; 312 AA.
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1850.
 PN WO200127158-A2.
 PD 19-APR-2001.
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 Query Match 5.9%; Score 71; DB 4; Length 312;
 Best Local Similarity 22.9%; Pred. No. 41;
 RESULT 1184
 ID AAG72377 standard; protein; 312 AA.
 DE Human OR-2-like polypeptide query sequence, SEQ ID NO: 2058.
 PN WO200127158-A2.
 PD 19-APR-2001.
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 Query Match 5.9%; Score 71; DB 4; Length 312;
 Best Local Similarity 22.9%; Pred. No. 41;
 RESULT 1185
 ID ADY08080 standard; protein; 364 AA.
 DE Plant full length insert polypeptide seqid 63895.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Query Match 5.9%; Score 71; DB 8; Length 364;
 Best Local Similarity 18.7%; Pred. No. 51;
 RESULT 1186
 ID AEF93343 standard; protein; 382 AA.
 DE Canis sphingosine-1-phosphate isoform 1 (cs1p1) receptor.
 PN WO2006014802-A2.
 PD 09-FEB-2006.
 PA (MERI) MERCK & CO INC.
 Query Match 5.9%; Score 71; DB 10; Length 382;
 Best Local Similarity 20.5%; Pred. No. 54;
 RESULT 1187
 ID ABB54394 standard; protein; 391 AA.
 DE Lactococcus lactis protein ykii.
 PN FR2807446-A1.
 PD 12-OCT-2001.
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 Query Match 5.9%; Score 71; DB 5; Length 391;
 Best Local Similarity 20.3%; Pred. No. 56;
 RESULT 1188
 ID ABB48413 standard; protein; 423 AA.
 DE Listeria monocytogenes protein #1117.
 PN WO200177335-A2.
 PD 18-OCT-2001.
 PA (INSP) INST PASTEUR.
 Query Match 5.9%; Score 71; DB 5; Length 423;
 Best Local Similarity 28.4%; Pred. No. 62;
 RESULT 1189
 ID ADL05302 standard; protein; 423 AA.
 DE M. catarrhalis protein #1068.
 PN US6673910-B1.
 PD 06-JAN-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 71; DB 8; Length 423;
 Best Local Similarity 38.0%; Pred. No. 62;
 RESULT 1190

PA (SATO/) SATO T.
Query Match
Best Local Similarity 5.9%; Score 71; DB 7; Length 471;
RESULT 1208
ID ADH14220 standard; protein; 471 AA.
DE Mutated human serotonin 5HT_2A.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match
Best Local Similarity 5.9%; Score 71; DB 7; Length 471;
RESULT 1209
ID ADH14114 standard; protein; 471 AA.
DE Human serotonin 5HT_2A.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match
Best Local Similarity 5.9%; Score 71; DB 7; Length 471;
RESULT 1210
ID ADL90125 standard; protein; 471 AA.
DE Human serotonin receptor 5HT2a.
PN US2003167476-A1.
PD 04-SEP-2003.
PA (CONK/) CONKLIN B R.
Query Match
Best Local Similarity 5.9%; Score 71; DB 7; Length 471;
RESULT 1211
ID ADO29506 standard; protein; 471 AA.
DE Human GPCR HTR2a, SEQ ID NO:608.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 5.9%; Score 71; DB 8; Length 471;
RESULT 1212
ID ADO39980 standard; protein; 471 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1463.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 5.9%; Score 71; DB 8; Length 471;
RESULT 1213
ID ADO39799 standard; protein; 471 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1462.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 5.9%; Score 71; DB 8; Length 471;
RESULT 1214
ID ADO39798 standard; protein; 471 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1461.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 5.9%; Score 71; DB 8; Length 471;
RESULT 1215
ID ADU48367 standard; protein; 471 AA.
DE Human serotonin 2A receptor protein.
PN US2004229287-A1.
PD 18-NOV-2004.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match
Best Local Similarity 5.9%; Score 71; DB 8; Length 471;
RESULT 1216
ID ADX02782 standard; protein; 471 AA.

DE Human 5-HT 2a receptor protein SeqID22.
PN WO2005012254-A1.
PD 10-FEB-2005.
PA (AREN-) ARENA PHARM INC.
Query Match
Best Local Similarity 5.9%; Score 71; DB 9; Length 471;
RESULT 1217
ID AEF70361 standard; protein; 471 AA.
DE Human 5-hydroxytryptamine 2A receptor protein sequence.
PN WO2006010515-A2.
PD 02-FEB-2006.
PA (FARB) BAYER HEALTHCARE AG.
Query Match
Best Local Similarity 5.9%; Score 71; DB 10; Length 471;
RESULT 1218
ID AAY01626 standard; protein; 478 AA.
DE Amino acid sequence of the human 5-HT2 receptor.
PN US5885785-A.
PD 23-MAR-1999.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match
Best Local Similarity 5.9%; Score 71; DB 2; Length 478;
RESULT 1219
ID ABG70577 standard; protein; 480 AA.
DE Human serotonin (5-HT2) receptor.
PN US2002098548-A1.
PD 25-JUL-2002.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match
Best Local Similarity 5.9%; Score 71; DB 5; Length 480;
RESULT 1220
ID ABW70440 standard; protein; 493 AA.
DE Photorhabdus luminescens protein sequence #3537.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 5.9%; Score 71; DB 6; Length 493;
RESULT 1221
ID ADE56383 standard; protein; 545 AA.
DE Rat Protein O70536, SEQ ID NO 2235.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 5.9%; Score 71; DB 7; Length 545;
RESULT 1222
ID ADD48660 standard; protein; 545 AA.
DE Rat Protein BMA25372, SEQ ID NO 14366.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
Query Match
Best Local Similarity 5.9%; Score 71; DB 7; Length 545;
RESULT 1223
ID ADS43584 standard; protein; 546 AA.
DE Bacterial polypeptide #22014.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match
Best Local Similarity 5.9%; Score 71; DB 8; Length 546;
RESULT 1224
ID ASJ26399 standard; protein; 559 AA.
DE Aspergillus fumigatus essential gene protein #1057.
PN WO200286090-A2.

PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 71; DB 6; Length 559;
Best Local Similarity 23.1%; Pred. No. 92;
RESULT 1225
ID ABP5686 standard; protein; 563 AA.
DE Fungal 28C protein sequence #112.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match 5.9%; Score 71; DB 5; Length 563;
Best Local Similarity 19.1%; Pred. No. 93;
RESULT 1226
ID AAB20578 standard; protein; 564 AA.
DE Mouse OCTN3 protein SEQ ID NO:1.
PN WO200046368-A1.
PD 10-AUG-2000.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.9%; Score 71; DB 3; Length 564;
Best Local Similarity 21.4%; Pred. No. 93;
RESULT 1227
ID AED51410 standard; protein; 564 AA.
DE Novel organic cation transporter (OCTN) protein, MOCTN3, SEQ ID NO: 83.
PN US2005241012-A1.
PD 27-OCT-2005.
PA (NIGA/) NIGAM S K.
PA (ERAL/) ERALY S A.
Query Match 5.9%; Score 71; DB 9; Length 564;
Best Local Similarity 21.4%; Pred. No. 93;
RESULT 1228
ID AEB36506 standard; protein; 603 AA.
DE L. pneumophila protein SEQ ID NO 838.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UJLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 71; DB 9; Length 603;
Best Local Similarity 18.3%; Pred. No. 1e+02;
RESULT 1229
ID ADQ96374 standard; protein; 631 AA.
DE T cell activation associated protein #276.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 5.9%; Score 71; DB 8; Length 631;
Best Local Similarity 21.3%; Pred. No. 1.1e+02;
RESULT 1230
ID ADQ96376 standard; protein; 631 AA.
DE T cell activation associated protein #277.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 5.9%; Score 71; DB 8; Length 631;
Best Local Similarity 21.3%; Pred. No. 1.1e+02;
RESULT 1231
ID ABB91532 standard; protein; 676 AA.
DE Herbicidally active polypeptide SEQ ID NO 743.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 71; DB 5; Length 676;
Best Local Similarity 22.3%; Pred. No. 1.2e+02;
RESULT 1232
ID AAE21800 standard; protein; 727 AA.
DE Human HIPHUM 0000029 protein.
PN GB2365432-A.
PD 20-FEB-2002.
PA (GLAX) GLAXO GROUP LTD.
Query Match 5.9%; Score 71; DB 5; Length 727;
Best Local Similarity 24.3%; Pred. No. 1.3e+02;
RESULT 1233
ID ABUE4636 standard; protein; 727 AA.
DE Human NOVX polypeptide #95.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 71; DB 6; Length 727;
Best Local Similarity 24.3%; Pred. No. 1.3e+02;
RESULT 1234
ID ADH76500 standard; protein; 727 AA.
DE 727 amino acid human neurotransmitter transporter protein.
PN US2003219774-A1.
PD 27-NOV-2003.
PA (SHAR/) SHARMA R.
PA (RAMA/) RAMANATHAN C S.
PA (WEST/) WESTPHAL R.
PA (FEDE/) FEDER J N.
PA (LEEL/) LEE L M.
Query Match 5.9%; Score 71; DB 8; Length 727;
Best Local Similarity 24.3%; Pred. No. 1.3e+02;
RESULT 1235
ID AEF1189 standard; protein; 742 AA.
DE HCV protein BP208/FLF SEQ ID NO:44.
PN WO2006001517-A1.
PD 05-JAN-2006.
PA (ADLI-) ADVANCED LIFE SCI INST INC.
Query Match 5.9%; Score 71; DB 10; Length 742;
Best Local Similarity 24.8%; Pred. No. 1.4e+02;
RESULT 1236
ID ABR62929 standard; protein; 744 AA.
DE Human neurotransmitter transporter.
PN WO2003059947-A1.
PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 71; DB 7; Length 744;
Best Local Similarity 24.3%; Pred. No. 1.4e+02;
RESULT 1237
ID ABB60052 standard; protein; 792 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6948.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.9%; Score 71; DB 4; Length 792;
Best Local Similarity 17.7%; Pred. No. 1.5e+02;
RESULT 1238
ID ABM90462 standard; protein; 929 AA.
DE Rice abiotic stress responsive polypeptide SEQ ID NO:9184.
PN WO2003008540-A2.
PD 30-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.9%; Score 71; DB 7; Length 929;
Best Local Similarity 20.6%; Pred. No. 1.9e+02;
RESULT 1239
ID AAR30616 standard; protein; 3010 AA.
DE Polypeptide coded by Korean HCV full cDNA sequence LBCL1.
PN RP521318-A2.
PD 07-JAN-1993.
PA (LUCK-) LUCKY LTD.
Query Match 5.9%; Score 71; DB 2; Length 3010;
Best Local Similarity 26.9%; Pred. No. 9.5e+02;
RESULT 1240
ID AAR53417 standard; protein; 3010 AA.
DE Blood transmissible NANBHV protein.
PN JP06105690-A.
PD 19-APR-1994.
PA (KAEN/) KAENNO K.
Query Match 5.9%; Score 71; DB 2; Length 3010;
Best Local Similarity 26.9%; Pred. No. 9.5e+02;
RESULT 1241
ID ADX40817 standard; protein; 3010 AA.
DE HCV polymerase protein #40.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIN-) EPIMMUNE INC.

Query Match
Best Local Similarity 5.9%; Score 71; DB 9; Length 3010;
RESULT 1242
ID ADX40783 standard; protein; 3010 AA.
DE HCV polymerase protein #6.
FN WC005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMUNE INC.

Query Match
Best Local Similarity 5.9%; Score 71; DB 9; Length 3010;
RESULT 1243
ID ADX40812 standard; protein; 3010 AA.
DE HCV polymerase protein #35.
FN WC005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMUNE INC.

Query Match
Best Local Similarity 5.9%; Score 71; DB 9; Length 3010;
RESULT 1244
ID ABR83573 standard; protein; 202 AA.
DE BcrC amino acid sequence SEQ ID NO:40.
FN WC0003057708-A2.
PD 17-JUL-2003.
PA (UYNE-) UNIV NEWCASTLE VENTURES LTD.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 6; Length 202;
RESULT 1245
ID AAU01287 standard; protein; 218 AA.
DE Brassica napus fatty acid desaturase, Fad3C, partial sequence.
FN WC000125453-A2.
PD 12-APR-2001.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 4; Length 218;
RESULT 1246
ID AAU97208 standard; protein; 228 AA.
DE Portion of a wheat sugar transport protein encoded by wreln.pk0006.b4.
FN US6383776-B1.
PD 07-MAY-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 5; Length 228;
RESULT 1247
ID ABU08333 standard; protein; 228 AA.
DE Wheat sugar transport protein #3.
FN US2002178468-A1.
PD 28-NOV-2002.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 6; Length 228;
RESULT 1248
ID ADG47920 standard; protein; 228 AA.
DE Wheat Arabidopsis-like sugar transport protein #3.
FN US2002198217-A1.
PD 26-DEC-2002.
PA (ALLE/) ALLEN S M.
PA (HITZ/) HITZ W D.
PA (KINN/) KINNEY A J.
PA (TING/) TINGEY S V.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 228;
RESULT 1249
ID ABE68531 standard; protein; 228 AA.
DE Triticum aestivum sugar transport protein amino acid sequence SEQ ID 16.
FN US2005282278-A1.
PD 22-DEC-2005.
PA (ALLE/) ALLEN S M.
PA (HITZ/) HITZ W D.
PA (KINN/) KINNEY A J.
PA (TING/) TINGEY S V.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 10; Length 228;
RESULT 1250
ID ABE68531 standard; protein; 228 AA.
DE Triticum aestivum sugar transport protein amino acid sequence SEQ ID 16.
FN US2005282278-A1.
PD 22-DEC-2005.
PA (ALLE/) ALLEN S M.
PA (HITZ/) HITZ W D.
PA (KINN/) KINNEY A J.
PA (TING/) TINGEY S V.

ID ABU17430 standard; protein; 275 AA.
DE Protein encoded by Prokaryotic essential gene #2957.
FN WC00277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 6; Length 275;
RESULT 1251
ID ADY06253 standard; protein; 283 AA.
DE Plant full length insert polypeptide seqid 62068.
FN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.

PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 283;
RESULT 1252
ID ABB55033 standard; protein; 285 AA.
DE Lactococcus lactis protein malG.
FN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 5; Length 285;
RESULT 1253
ID ABB05467 standard; protein; 291 AA.
DE Coriolus versicolor aldo/ketoreductase protein SEQ ID NO:2.
FN JP2001321171-A.
PD 20-NOV-2001.
PA (WARI/) WARIISHI H.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 5; Length 291;
RESULT 1254
ID ADA35787 standard; protein; 297 AA.
DE Acinetobacter baumannii protein #2948.
FN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 6; Length 297;
RESULT 1255
ID AEM70358 standard; protein; 321 AA.
DE Photorhabdus luminescens protein sequence #3455.
FN WC00294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 6; Length 321;
RESULT 1256
ID ADH22355 standard; protein; 330 AA.
DE Human receptor & membrane associated protein (REMAP) SeqID5.
FN WC0003104395-A2.
PD 18-DEC-2003.
PA (INCY-) INCYTE CORP.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 330;
RESULT 1257
ID ADK68232 standard; protein; 343 AA.
DE Novel NOVX protein #79.
FN WC0003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.

Query Match
Best Local Similarity 5.9%; Score 70.5; DB 7; Length 343;
RESULT 1258
ID ADH72226 standard; protein; 343 AA.
DE Human protein of the invention NOV55a SEQ ID NO:1122.

PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.9%; Score 70.5; DB 8; Length 343;
 Best Local Similarity 30.0%; Pred. No. 53;
 RESULT 1259
 ID ADR49221 standard; protein; 343 AA.
 DE Human NOV10a protein.
 PN US2004162236-A1.
 PD 19-AUG-2004.
 PA (ALSO-) ALSOBROOK J.
 PA (BENT-) BENTO P.
 PA (BOLD-) BOLDOG F.
 PA (BURG-) BURGESS C.
 PA (CASM-) CASMAN S.
 PA (BOKO-) BOKOR J C.
 PA (EDIN-) EDINGER S R.
 PA (ELLE-) ELLERMAN K.
 PA (FERN-) FERNANDES E.
 PA (GERL-) GERLACH V.
 PA (GROS-) GROSSE W.
 PA (GUNT-) GUNTHER E.
 PA (GUSE-) GUSEV V.
 PA (HEYE-) HEYES M.
 PA (LEPL-) LEPLEY D.
 PA (LILL-) LI L.
 PA (MACD-) MACDOUGALL J R.
 PA (MALY-) MALLYANKAR U M.
 PA (MILL-) MILLET I.
 PA (PATY-) PATTURAJAN M.
 PA (PEYM-) PEYMAN J A.
 PA (RAST-) RASTELLI L.
 PA (RIEG-) RIEGER D.
 PA (SHEN-) SHENOY S.
 PA (SHIM-) SHIMKETS R.
 PA (SMIT-) SMITHSON G.
 PA (STON-) STONE D.
 PA (VERN-) VERNET C.
 PA (VOSS-) VOSS E.
 Query Match 5.9%; Score 70.5; DB 8; Length 343;
 Best Local Similarity 30.0%; Pred. No. 53;
 RESULT 1260
 ID ADY15182 standard; protein; 350 AA.
 DE PRO polypeptide SEQ ID NO 988.
 PN WO2005016962-A2.
 PD 24-FEB-2005.
 PA (GETH-) GENENTECH INC.
 Query Match 5.9%; Score 70.5; DB 9; Length 350;
 Best Local Similarity 18.5%; Pred. No. 55;
 RESULT 1261
 ID ADY15180 standard; protein; 350 AA.
 DE PRO polypeptide SEQ ID NO 986.
 PN WO2005016962-A2.
 PD 24-FEB-2005.
 PA (GETH-) GENENTECH INC.
 Query Match 5.9%; Score 70.5; DB 9; Length 350;
 Best Local Similarity 18.5%; Pred. No. 55;
 RESULT 1262
 ID ADR40543 standard; protein; 363 AA.
 DE Ovine melatonin receptor O46608 protein.
 PN US2004161823-A1.
 PD 19-AUG-2004.
 PA (FEDE-) FEDER J N.
 PA (MINT-) MINTIER G.
 PA (RAMA-) RAMANATHAN C S.
 PA (HAWK-) HAWKEN D R.
 Query Match 5.9%; Score 70.5; DB 8; Length 363;
 Best Local Similarity 23.1%; Pred. No. 58;
 RESULT 1263
 ID AAR69518 standard; protein; 365 AA.
 DE Prostaglandin-EP3-9 receptor.
 PN WO9500552-A1.
 PD 05-JAN-1995.

PA (MERI-) MERCK FROSST CANADA INC.
 Query Match 5.9%; Score 70.5; DB 2; Length 365;
 Best Local Similarity 24.2%; Pred. No. 58;
 RESULT 1264
 ID AAE38521 standard; protein; 365 AA.
 DE Human PTGER3 protein isoform, EP3b.
 PN WO2003064471-A2.
 PD 07-AUG-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 7; Length 365;
 Best Local Similarity 24.2%; Pred. No. 58;
 RESULT 1265
 ID ADI35077 standard; protein; 365 AA.
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #9.
 PN US2003224393-A1.
 PD 04-DEC-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 8; Length 365;
 Best Local Similarity 24.2%; Pred. No. 58;
 RESULT 1266
 ID ADL15889 standard; protein; 365 AA.
 DE Human prostaglandin EP3 receptor #3.
 PN US6670134-B1.
 PD 30-DEC-2003.
 PA (ALLR-) ALLERGAN INC.
 Query Match 5.9%; Score 70.5; DB 8; Length 365;
 Best Local Similarity 24.2%; Pred. No. 58;
 RESULT 1267
 ID ADR67864 standard; protein; 365 AA.
 DE Prostaglandin E2 EP3 III.
 PN WO2004074830-A2.
 PD 02-SEP-2004.
 PA (FARB-) BAYER HEALTHCARE AG.
 Query Match 5.9%; Score 70.5; DB 8; Length 365;
 Best Local Similarity 24.2%; Pred. No. 58;
 RESULT 1268
 ID ADS21429 standard; protein; 366 AA.
 DE Bacterial polypeptide #10462.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY-) CAO Y.
 PA (HINK-) HINKLE G J.
 PA (SLAT-) SLATER S C.
 PA (CHEN-) CHEN X.
 PA (GOLD-) GOLDMAN B S.
 Query Match 5.9%; Score 70.5; DB 8; Length 366;
 Best Local Similarity 21.2%; Pred. No. 58;
 RESULT 1269
 ID ADF04358 standard; protein; 367 AA.
 DE Bacterial polypeptide #471.
 PN US6605709-B1.
 PD 12-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 70.5; DB 7; Length 367;
 Best Local Similarity 33.3%; Pred. No. 59;
 RESULT 1270
 ID AAE38520 standard; protein; 374 AA.
 DE Human PTGER3 protein isoform, EP3d.
 PN WO2003064471-A2.
 PD 07-AUG-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 7; Length 374;
 Best Local Similarity 24.2%; Pred. No. 60;
 RESULT 1271
 ID ADI35075 standard; protein; 374 AA.
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #8.
 PN US2003224393-A1.
 PD 04-DEC-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 8; Length 374;
 Best Local Similarity 24.2%; Pred. No. 60;
 RESULT 1272

ID AAR48711 standard; protein; 379 AA.
DE G-protein coupled rat serotonin 2 receptor protein.
FN WO9405695-A1.
PD 17-MAR-1994.
PA (UNYNY) UNIV NEW YORK STATE.
Query Match 5.9%; Score 70.5; DB 2; Length 379;
Best Local Similarity 22.9%; Pred. No. 61;
RESULT 1273
ID AAW02683 standard; peptide; 379 AA.
DE G-protein coupled rat serotonin 2 receptor.
FN US5508384-A.
PD 16-APR-1996.
PA (UNYNY) UNIV NEW YORK STATE.
Query Match 5.9%; Score 70.5; DB 2; Length 379;
Best Local Similarity 22.9%; Pred. No. 61;
RESULT 1274
ID AAR69517 standard; protein; 388 AA.
DE Prostaglandin-EP3-21 receptor.
FN WO9500552-A1.
PD 05-JAN-1995.
PA (MERI) MERCK FROSST CANADA INC.
Query Match 5.9%; Score 70.5; DB 2; Length 388;
Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1275
ID AAE38513 standard; protein; 388 AA.
DE Human PTGER3 protein isoform, EP3c.
FN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 388;
Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1276
ID ADI35061 standard; protein; 388 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #1.
FN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 388;
Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1277
ID ADI5887 standard; protein; 388 AA.
DE Human prostaglandin EP3 receptor #2.
FN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR) ALLERGAN INC.
PA (UYAR-) UNIV ARIZONA.
Query Match 5.9%; Score 70.5; DB 8; Length 388;
Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1278
ID ADS13753 standard; protein; 388 AA.
DE Human prostaglandin E2 EP3 II polypeptide.
FN WO2004075813-A2.
PD 10-SEP-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 5.9%; Score 70.5; DB 8; Length 388;
Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1279
ID AAR69516 standard; protein; 390 AA.
DE Prostaglandin-EP3-alpha receptor.
FN WO9500552-A1.
PD 05-JAN-1995.
PA (MERI) MERCK FROSST CANADA INC.
Query Match 5.9%; Score 70.5; DB 2; Length 390;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1280
ID AAE38516 standard; protein; 390 AA.
DE Human PTGER3 protein isoform, EP3a1.
FN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 390;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1281

ID AAE38517 standard; protein; 390 AA.
DE Human PTGER3 protein isoform, EP3a2.
FN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 390;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1282
ID ADI35067 standard; protein; 390 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #4.
FN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1283
ID ADI35069 standard; protein; 390 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #5.
FN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1284
ID ADI15898 standard; protein; 390 AA.
DE Human prostaglandin EP3 receptor #4.
FN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR) ALLERGAN INC.
PA (UYAR-) UNIV ARIZONA.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1285
ID ADI15885 standard; protein; 390 AA.
DE Human prostaglandin EP3 receptor #1.
FN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR) ALLERGAN INC.
PA (UYAR-) UNIV ARIZONA.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1286
ID ADR70434 standard; protein; 390 AA.
DE Human prostaglandin E2 EP3 protein.
FN WO2004074842-A2.
PD 02-SEP-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1287
ID ADS76168 standard; protein; 390 AA.
DE Prostaglandin E2 EP3 I.
FN WO2004075814-A2.
PD 10-SEP-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1288
ID AEF06389 standard; protein; 390 AA.
DE Human PGE receptor type 3a2 SEQ ID NO 7.
FN WO2005085851-A2.
PD 15-SEP-2005.
PA (ADRA/) ADRA C N.
Query Match 5.9%; Score 70.5; DB 10; Length 390;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1289
ID AAW57411 standard; protein; 393 AA.
DE Human prostaglandin EP3-VI receptor.
FN JF10113185-A.
PD 06-MAY-1998.
PA (ONOO) ONO PHARM CO LTD.
Query Match 5.9%; Score 70.5; DB 2; Length 393;
Best Local Similarity 24.2%; Pred. No. 65;

RESULT 1290
ID AAE38519 standard; protein; 393 AA.
DE Human PTGER3 protein isoform, EP3e.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 393;
Best Local Similarity 24.2%; Pred. No. 65;
RESULT 1291
ID AAE38523 standard; protein; 393 AA.
DE Human PTGER3 protein isoform, EP3-VI.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 393;
Best Local Similarity 24.2%; Pred. No. 65;
RESULT 1292
ID ADI35081 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 65;
RESULT 1293
ID ADI35073 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 65;
RESULT 1294
ID AAW57410 standard; protein; 402 AA.
DE Human EP3-V receptor.
PN JP10113185-A.
PD 06-MAY-1998.
PA (ONOY) ONO PHARM CO LTD.
Query Match 5.9%; Score 70.5; DB 2; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1295
ID ABP81904 standard; protein; 402 AA.
DE Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.9%; Score 70.5; DB 6; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1296
ID AAE38522 standard; protein; 402 AA.
DE Human PTGER3 protein isoform, EP3-V.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1297
ID ADI35079 standard; protein; 402 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1298
ID ADO35167 standard; protein; 402 AA.
DE Protein #69 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1299
ID AAE38519 standard; protein; 393 AA.
DE Human PTGER3 protein isoform, EP3e.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 393;
Best Local Similarity 24.2%; Pred. No. 65;
RESULT 1291
ID AAE38523 standard; protein; 393 AA.
DE Human PTGER3 protein isoform, EP3-VI.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 393;
Best Local Similarity 24.2%; Pred. No. 65;
RESULT 1292
ID ADI35081 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 65;
RESULT 1293
ID ADI35073 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 65;
RESULT 1294
ID AAW57410 standard; protein; 402 AA.
DE Human EP3-V receptor.
PN JP10113185-A.
PD 06-MAY-1998.
PA (ONOY) ONO PHARM CO LTD.
Query Match 5.9%; Score 70.5; DB 2; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1295
ID ABP81904 standard; protein; 402 AA.
DE Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.9%; Score 70.5; DB 6; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1296
ID AAE38522 standard; protein; 402 AA.
DE Human PTGER3 protein isoform, EP3-V.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1297
ID ADI35079 standard; protein; 402 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1298
ID ADO35167 standard; protein; 402 AA.
DE Protein #69 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1299
ID AAE38519 standard; protein; 393 AA.
DE Human PTGER3, SEQ ID NO:722.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1300
ID ADZ09834 standard; protein; 402 AA.
DE Human breast cancer marker DKFZp586M0723 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 5.9%; Score 70.5; DB 9; Length 402;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1301
ID AAE38514 standard; protein; 407 AA.
DE Human PTGER3 protein isoform, EP3g.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 407;
Best Local Similarity 24.2%; Pred. No. 68;
RESULT 1302
ID ADI35063 standard; protein; 407 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #2.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 407;
Best Local Similarity 24.2%; Pred. No. 68;
RESULT 1303
ID AAE38518 standard; protein; 425 AA.
DE Human PTGER3 protein isoform, EP3f.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 425;
Best Local Similarity 24.2%; Pred. No. 72;
RESULT 1304
ID ADI35071 standard; protein; 425 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #6.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 425;
Best Local Similarity 24.2%; Pred. No. 72;
RESULT 1305
ID AEF77677 standard; protein; 425 AA.
DE Human prostaglandin E receptor 2 (PTGER2) variant 1.
PN WO2006017171-A2.
PD 16-FEB-2006.
PA (META-) METABOLEX INC.
Query Match 5.9%; Score 70.5; DB 10; Length 425;
Best Local Similarity 24.2%; Pred. No. 72;
RESULT 1306
ID AAE38515 standard; protein; 433 AA.
DE Human PTGER3 protein isoform, EP3h.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 433;
Best Local Similarity 24.2%; Pred. No. 74;
RESULT 1307
ID ADI35065 standard; protein; 433 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 433;
Best Local Similarity 24.2%; Pred. No. 74;
RESULT 1308
ID AAW98431 standard; protein; 480 AA.

DE H. pylori GHPO 446 protein.
 PN W09843478-A1.
 PD 08-OCT-1998.
 PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 480;
 PD 23.1%; Pred. No. 85;
 RESULT 1309
 ID ADY09805 standard; protein; 494 AA.
 DE Plant full length insert polypeptide seqid 65620.
 PN US2004034888-A1.
 PD 19-FEB-2004.
 PA (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 494;
 PD 21.4%; Pred. No. 89;
 RESULT 1310
 ID ABP40525 standard; protein; 499 AA.
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5370.
 PN US6380370-B1.
 PD 30-APR-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 499;
 PD 20.5%; Pred. No. 90;
 RESULT 1311
 ID ADS06092 standard; protein; 499 AA.
 DE Staphylococcus epidermidis polypeptide seqid 5387.
 PN US2004147734-A1.
 PD 29-JUL-2004.
 PA (DOUC/) DOUCETTE-STAMM L.
 PA (BUSH/) BUSH D.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 499;
 PD 20.5%; Pred. No. 90;
 RESULT 1312
 ID ABU30473 standard; protein; 521 AA.
 DE Protein encoded by Prokaryotic essential gene #16000.
 PN W0200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 6; Length 521;
 PD 23.7%; Pred. No. 95;
 RESULT 1313
 ID AAU97213 standard; protein; 539 AA.
 DE Wheat sugar transport protein encoded by wlk8.pk0001.a11.
 PN US6383776-B1.
 PD 07-MAY-2002.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 539;
 PD 26.0%; Pred. No. 1e+02;
 RESULT 1314
 ID ABU08338 standard; protein; 539 AA.
 DE Wheat sugar transport protein #4.
 PN US2002178468-A1.
 PD 28-NOV-2002.
 PA (ALLE/) ALLEN S M.
 PA (HITZ/) HITZ W D.
 PA (KINN/) KINNEY A J.
 PA (TING/) TINGEY S V.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 6; Length 539;
 PD 26.0%; Pred. No. 1e+02;
 RESULT 1315
 ID ADG47930 standard; protein; 539 AA.
 DE Wheat Beta-vulgaris-like sugar transport protein #1.
 PN US2002199217-A1.
 PD 26-DEC-2002.
 PA (HELE/) HELENTJARIIS T G.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 539;
 PD 26.0%; Pred. No. 1e+02;
 RESULT 1316

DE ABE68541 standard; protein; 539 AA.
 DE Triticum aestivum sugar transport protein amino acid sequence SEQ ID 26.
 PN US2005282278-A1.
 PD 22-DEC-2005.
 PA (ALLE/) ALLEN S M.
 PA (HITZ/) HITZ W D.
 PA (KINN/) KINNEY A J.
 PA (TING/) TINGEY S V.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 10; Length 539;
 PD 26.0%; Pred. No. 1e+02;
 RESULT 1317
 ID ABU27418 standard; protein; 548 AA.
 DE Protein encoded by Prokaryotic essential gene #12945.
 PN W0200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 6; Length 548;
 PD 24.0%; Pred. No. 1e+02;
 RESULT 1318
 ID ADN22789 standard; protein; 556 AA.
 DE Bacterial polypeptide #5442.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 556;
 PD 21.1%; Pred. No. 1e+02;
 RESULT 1319
 ID ADD46023 standard; protein; 599 AA.
 DE Rat Protein P23978, SEQ ID NO 11695.
 PN W02003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 599;
 PD 20.1%; Pred. No. 1.2e+02;
 RESULT 1320
 ID ABW02687 standard; protein; 599 AA.
 DE Rattus norvegicus neuronal GABA transporter (GAT-1).
 PN US2003143729-A1.
 PD 31-JUL-2003.
 PA (SYNA-) SYNAPTIC PHARM CORP.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 599;
 PD 20.1%; Pred. No. 1.2e+02;
 RESULT 1321
 ID AAM78767 standard; protein; 600 AA.
 DE Human protein SEQ ID NO 1429.
 PN W0200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 4; Length 600;
 PD 19.5%; Pred. No. 1.2e+02;
 RESULT 1322
 ID ADJ64315 standard; protein; 662 AA.
 DE Cartilage differentiation inhibiting protein, SEQ ID 10.
 PN W02004013326-A1.
 PD 12-FEB-2004.
 PA (ASAH) ASAH KASEI KK.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 662;
 PD 22.7%; Pred. No. 1.3e+02;
 RESULT 1323
 ID ABB92892 standard; protein; 700 AA.
 DE Herbicidally active polypeptide SEQ ID NO 2103.
 PN W0200210210-A2.
 PD 07-FEB-2002.
 PA (FARB) BAYER AG.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 700;
 PD 25.8%; Pred. No. 1.4e+02;
 RESULT 1324
 ID AAB56721 standard; protein; 717 AA.

DE Human prostate cancer antigen protein sequence SEQ ID NO:1299.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 5.9%; Score 70.5; DB 3; Length 717;
Best Local Similarity 22.4%; Pred. No. 1.5e+02;
RESULT 1325
ID ADG47941 standard; protein; 740 AA.
DE Arabidopsis thaliana-like sugar transport protein #2.
PN US2002199217-A1.
PD 26-DEC-2002.
PA (HELE/) HELENTARIS T G.
Query Match 5.9%; Score 70.5; DB 8; Length 740;
Best Local Similarity 22.8%; Pred. No. 1.6e+02;
RESULT 1326
ID AAG39555 standard; protein; 766 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48959.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70.5; DB 3; Length 766;
Best Local Similarity 21.3%; Pred. No. 1.6e+02;
RESULT 1327
ID AAG39554 standard; protein; 815 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48958.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70.5; DB 3; Length 815;
Best Local Similarity 21.3%; Pred. No. 1.8e+02;
RESULT 1328
ID AAG39553 standard; protein; 927 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48957.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70.5; DB 3; Length 927;
Best Local Similarity 21.3%; Pred. No. 2.1e+02;
RESULT 1329
ID ABP73754 standard; protein; 1026 AA.
DE Candida albicans essential protein SEQ ID NO 7591.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70.5; DB 5; Length 1026;
Best Local Similarity 22.3%; Pred. No. 2.4e+02;
RESULT 1330
ID AAW17057 standard; protein; 1027 AA.
DE Candida albicans chitin synthase (CHS1).
PN WO9716540-A1.
PD 09-MAY-1997.
PA (CHEM-) CHEMGENICS PHARM INC.
Query Match 5.9%; Score 70.5; DB 2; Length 1027;
Best Local Similarity 22.3%; Pred. No. 2.4e+02;
RESULT 1331
ID ADH22510 standard; protein; 1147 AA.
DE Human transporter & ion channel (TRICH) protein SeqID8.
PN WO2003093444-A2.
PD 13-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 5.9%; Score 70.5; DB 8; Length 1147;
Best Local Similarity 19.5%; Pred. No. 2.9e+02;
RESULT 1332
ID ADK18350 standard; protein; 1163 AA.
DE Human NOVX protein #2.
PN WO2003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 70.5; DB 7; Length 1163;
Best Local Similarity 19.5%; Pred. No. 2.9e+02;
RESULT 1333
ID ADM29274 standard; protein; 1163 AA.
DE Human novel protein NOV2b.
PN WO2003064628-A2.
PD 07-AUG-2003.

PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 70.5; DB 7; Length 1163;
Best Local Similarity 19.5%; Pred. No. 2.9e+02;
RESULT 1334
ID AAW53863 standard; peptide; 1780 AA.
DE Human gravin polypeptide.
PN US5741890-A.
PD 21-APR-1998.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match 5.9%; Score 70.5; DB 2; Length 1780;
Best Local Similarity 34.8%; Pred. No. 5.2e+02;
RESULT 1335
ID AAB15380 standard; protein; 1780 AA.
DE Human gravin protein sequence.
PN US6090929-A.
PD 18-JUL-2000.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match 5.9%; Score 70.5; DB 3; Length 1780;
Best Local Similarity 34.8%; Pred. No. 5.2e+02;
RESULT 1336
ID AAO17365 standard; protein; 1781 AA.
DE Human gravin.
PN EP1191107-A2.
PD 27-MAR-2002.
PA (SCHD-) SCHERING AG.
Query Match 5.9%; Score 70.5; DB 5; Length 1781;
Best Local Similarity 34.8%; Pred. No. 5.2e+02;
RESULT 1337
ID ABU03477 standard; protein; 1781 AA.
DE Angiogenesis-associated human protein sequence #22.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (BOEB-) EOS BIOTECHNOLOGY INC.
Query Match 5.9%; Score 70.5; DB 6; Length 1781;
Best Local Similarity 34.8%; Pred. No. 5.2e+02;
RESULT 1338
ID ABB97448 standard; protein; 1783 AA.
DE Novel human protein SEQ ID NO: 716.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70.5; DB 5; Length 1783;
Best Local Similarity 34.8%; Pred. No. 5.3e+02;
RESULT 1339
ID ABG21018 standard; protein; 1795 AA.
DE Novel human diagnostic protein #21009.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70.5; DB 4; Length 1795;
Best Local Similarity 34.8%; Pred. No. 5.3e+02;
RESULT 1340
ID AAG34242 standard; protein; 185 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 41631.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 185;
Best Local Similarity 26.2%; Pred. No. 26;
RESULT 1341
ID AAG34241 standard; protein; 189 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 41630.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.9%; Score 70; DB 3; Length 189;
Best Local Similarity 26.2%; Pred. No. 27;
RESULT 1342
ID AAW44944 standard; protein; 225 AA.
DE Avian infectious bronchitis virus glycoprotein M.
PN FR2751225-A1.
PD 23-JAN-1998.
PA (INMR-) RHONE MERIEUX SA.
Query Match 5.9%; Score 70; DB 2; Length 225;
Best Local Similarity 21.6%; Pred. No. 34;

DE Screening method related protein #1.
PN WO200293161-A1.
PD 21-NOV-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 6; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1362
ID ABR37874 standard; protein; 333 AA.
DE GPR7 ligand related human protein SEQ ID NO 84.
PN WO2002102847-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 6; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1363
ID ABR81897 standard; protein; 333 AA.
DE Human G protein-coupled receptor GPR8 protein SEQ ID NO:279.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.9%; Score 70; DB 6; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1364
ID ABR57245 standard; protein; 333 AA.
DE Human GPR8 protein SEQ ID NO:84.
PN WO2003045994-A1.
PD 05-JUN-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1365
ID ADC22691 standard; protein; 333 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #44.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1366
ID ADC22535 standard; protein; 333 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #5.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1367
ID ADC51793 standard; protein; 333 AA.
DE Human GPR8, SEQ ID 4.
PN WO2003057236-A1.
PD 17-JUL-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1368
ID ABR61545 standard; protein; 333 AA.
DE Human GPR8 receptor polypeptide.
PN WO2003081234-A2.
PD 02-OCT-2003.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1369
ID ADG41976 standard; protein; 333 AA.
DE Human GPR8 polypeptide.
PN JP2003009867-A.
PD 14-JAN-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1370
ID ADH14008 standard; protein; 333 AA.
DE Human GPR8.

PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1371
ID ADH14164 standard; protein; 333 AA.
DE Mutated human GPR8.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1372
ID ADG12852 standard; protein; 333 AA.
DE Human wild-type hGPR8 amino acid sequence SEQ ID NO:75.
PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1373
ID ADO29700 standard; protein; 333 AA.
DE Human GPCR GPR8, SEQ ID NO:802.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1374
ID ADO31044 standard; protein; 333 AA.
DE Human GPR8 protein SEQ ID NO:73.
PN WO2004041301-A1.
PD 21-MAY-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1375
ID ADO19919 standard; protein; 333 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1376
ID ADS14162 standard; protein; 333 AA.
DE Human GPR8 ligand protein SeqID 73.
PN WO2004080485-A1.
PD 23-SEP-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1377
ID ADV24041 standard; protein; 333 AA.
DE Neuropeptide W antibody associated polypeptide seqid 17.
PN WO2004106382-A1.
PD 09-DEC-2004.
PA (TAKE) TAKEDA PHARM CO LTD.
Query Match 5.9%; Score 70; DB 9; Length 333;
Best Local Similarity 23.6%; Pred. No. 59;
RESULT 1378
ID ADG12854 standard; protein; 347 AA.
DE Human HA tagged wild-type hGPR8 amino acid sequence SEQ ID NO:77.
PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 347;
Best Local Similarity 23.6%; Pred. No. 62;

RESULT 1379
ID ABG30839 standard; protein; 364 AA.
DE Human calcium channel protein.
PN WO200252003-A2.
PD 04-JUL-2002.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 70; DB 5; Length 364;
Best Local Similarity 25.0%; Pred. No. 66;
RESULT 1380
ID ADG12856 standard; protein; 364 AA.
DE Human hGPR8-enhanced receptor amino acid sequence SEQ ID NO:79.
PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 364;
Best Local Similarity 23.6%; Pred. No. 66;
RESULT 1381
ID ADO28778 standard; protein; 364 AA.
DE Human GPR8-enhanced receptor.
PN US2004091946-A1.
PD 13-MAY-2004.
PA (OAKL/) OAKLEY R H.
PA (BARA/) BARAK L S.
PA (LAPO/) LAPORTE S A.
PA (CARO/) CARON M G.
Query Match 5.9%; Score 70; DB 8; Length 364;
Best Local Similarity 23.6%; Pred. No. 66;
RESULT 1382
ID ADX44597 standard; protein; 364 AA.
DE Enhanced human G-protein coupled receptor 8 - SEQ ID 56.
PN WO2005012876-A2.
PD 10-FEB-2005.
PA (NORA-) NORAK BIOSCIENCES INC.
Query Match 5.9%; Score 70; DB 9; Length 364;
Best Local Similarity 23.6%; Pred. No. 66;
RESULT 1383
ID ADY83827 standard; protein; 364 AA.
DE hGPR8-enhanced receptor.
PN WO2005029035-A2.
PD 31-MAR-2005.
PA (NORA-) NORAK BIOSCIENCES INC.
Query Match 5.9%; Score 70; DB 9; Length 364;
Best Local Similarity 23.6%; Pred. No. 66;
RESULT 1384
ID ADG12858 standard; protein; 378 AA.
DE HA tagged hGPR8-enhanced receptor amino acid sequence SEQ ID NO:81.
PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 378;
Best Local Similarity 23.6%; Pred. No. 70;
RESULT 1385
ID ADN49121 standard; protein; 388 AA.
DE Mouse oxytocin receptor protein.
PN US2004086881-A1.
PD 06-MAY-2004.
PA (RAMA/) RAMANATHAN C S.
PA (GOPA/) GOPAL S.
PA (MINT/) MINTIER G A.
PA (FEDE/) FEDER J.
Query Match 5.9%; Score 70; DB 8; Length 388;
Best Local Similarity 24.8%; Pred. No. 73;
RESULT 1386
ID ADO29591 standard; protein; 388 AA.
DE Mouse GPCR OXTR, SEQ ID NO:693.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70; DB 8; Length 388;
Best Local Similarity 24.8%; Pred. No. 73;
RESULT 1387
ID ADA54410 standard; protein; 399 AA.
DE Human protein, SEQ ID 1978.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.9%; Score 70; DB 6; Length 399;
Best Local Similarity 22.9%; Pred. No. 75;
RESULT 1388
ID ABG99947 standard; protein; 399 AA.
DE Human novel polypeptide #60.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70; DB 6; Length 399;
Best Local Similarity 22.9%; Pred. No. 75;
RESULT 1389
ID ADC96947 standard; protein; 425 AA.
DE E. faecium protein sequence SEQ ID 6574.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 7; Length 425;
Best Local Similarity 25.9%; Pred. No. 82;
RESULT 1390
ID ADA34110 standard; protein; 470 AA.
DE Acinetobacter baumannii protein #1271.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 6; Length 470;
Best Local Similarity 23.5%; Pred. No. 95;
RESULT 1391
ID ABM67264 standard; protein; 474 AA.
DE Photorhabdus luminescens protein sequence #361.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 6; Length 474;
Best Local Similarity 22.9%; Pred. No. 96;
RESULT 1392
ID AAE16787 standard; protein; 475 AA.
DE Human transporter and ion channel-24 (TRICH-24) protein.
PN WO200192304-A2.
PD 06-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.9%; Score 70; DB 5; Length 475;
Best Local Similarity 25.0%; Pred. No. 96;
RESULT 1393
ID ADA89683 standard; protein; 506 AA.
DE Staphylococcus aureus antigenic protein #222.
PN WO2003011899-A2.
PD 13-FEB-2003.
PA (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSYNEXUS INC.
Query Match 5.9%; Score 70; DB 6; Length 506;
Best Local Similarity 20.1%; Pred. No. 1e+02;
RESULT 1394
ID ABW72414 standard; protein; 506 AA.
DE Staphylococcus aureus protein #1654.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.9%; Score 70; DB 6; Length 506;
Best Local Similarity 20.1%; Pred. No. 1e+02;
RESULT 1395
ID AAE21176 standard; protein; 540 AA.
DE Human TRICH-20 protein.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.9%; Score 70; DB 5; Length 540;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
RESULT 1396

ID AAM39017 standard; protein; 552 AA.
DE Human polypeptide SEQ ID NO 2162.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70; DB 4; Length 552;
Best Local Similarity 25.0%; Pred. No. 1.2e+02;
RESULT 1397
ID ABU18262 standard; protein; 602 AA.
DE Protein encoded by Prokaryotic essential gene #3789.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70; DB 6; Length 602;
Best Local Similarity 26.4%; Pred. No. 1.3e+02;
RESULT 1398
ID ABU33453 standard; protein; 637 AA.
DE Protein encoded by Prokaryotic essential gene #18980.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70; DB 6; Length 637;
Best Local Similarity 23.1%; Pred. No. 1.4e+02;
RESULT 1399
ID AEB39900 standard; protein; 637 AA.
DE L. pneumophila protein SEQ ID NO 4232.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 9; Length 637;
Best Local Similarity 22.3%; Pred. No. 1.4e+02;
RESULT 1400
ID AAY91335 standard; protein; 640 AA.
DE Group B Streptococcus protein sequence SEQ ID NO:68.
PN WO200006736-A2.
PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNIQS LTD.
Query Match 5.9%; Score 70; DB 3; Length 640;
Best Local Similarity 21.4%; Pred. No. 1.5e+02;
RESULT 1401
ID AEB36499 standard; protein; 647 AA.
DE L. pneumophila protein SEQ ID NO 831.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 9; Length 647;
Best Local Similarity 22.3%; Pred. No. 1.5e+02;
RESULT 1402
ID AEM83618 standard; protein; 695 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4067.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.9%; Score 70; DB 8; Length 695;
Best Local Similarity 28.6%; Pred. No. 1.6e+02;
RESULT 1403
ID ADL04660 standard; protein; 767 AA.
DE M. catarrhalis protein #426.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 8; Length 767;
Best Local Similarity 21.3%; Pred. No. 1.9e+02;
RESULT 1404
ID AAR53921 standard; protein; 980 AA.
DE HCV fusion protein corresp. to N-terminal of ORF.
PN JF06092996-A.

PD 05-APR-1994.
PA (SHIM/) SHIMOTOYA K.
Query Match 5.9%; Score 70; DB 2; Length 980;
Best Local Similarity 24.6%; Pred. No. 2.6e+02;
RESULT 1405
ID ADS24062 standard; protein; 1041 AA.
DE Bacterial polypeptide #13095.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 70; DB 8; Length 1041;
Best Local Similarity 23.4%; Pred. No. 2.9e+02;
RESULT 1406
ID ADU69762 standard; protein; 1049 AA.
DE S agalactiae hyperimmune serum reactive antigen seqid 457.
PN WO2004099242-A2.
PD 18-NOV-2004.
PA (INTE-) INTERCELL AG.
Query Match 5.9%; Score 70; DB 8; Length 1049;
Best Local Similarity 18.8%; Pred. No. 2.9e+02;
RESULT 1407
ID ADU69581 standard; protein; 1049 AA.
DE S agalactiae hyperimmune serum reactive antigen seqid 276.
PN WO2004099242-A2.
PD 18-NOV-2004.
PA (INTE-) INTERCELL AG.
Query Match 5.9%; Score 70; DB 8; Length 1049;
Best Local Similarity 18.8%; Pred. No. 2.9e+02;
RESULT 1408
ID ADU69756 standard; protein; 1049 AA.
DE S agalactiae hyperimmune serum reactive antigen seqid 451.
PN WO2004099242-A2.
PD 18-NOV-2004.
PA (INTE-) INTERCELL AG.
Query Match 5.9%; Score 70; DB 8; Length 1049;
Best Local Similarity 18.8%; Pred. No. 2.9e+02;
RESULT 1409
ID ADV87847 standard; protein; 1049 AA.
DE Streptococcus agalactiae protein sequence, SEQ ID 241.
PN FR2824074-A1.
PD 31-OCT-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 8; Length 1049;
Best Local Similarity 18.8%; Pred. No. 2.9e+02;
RESULT 1410
ID ADV79100 standard; protein; 1049 AA.
DE Streptococcus agalactiae protein, SEQ ID 241.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 8; Length 1049;
Best Local Similarity 18.8%; Pred. No. 2.9e+02;
RESULT 1411
ID ADV82666 standard; protein; 1049 AA.
DE Streptococcus agalactiae protein, SEQ ID 3807.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 8; Length 1049;
Best Local Similarity 18.8%; Pred. No. 2.9e+02;
RESULT 1412
ID ADV81299 standard; protein; 1049 AA.
DE Streptococcus agalactiae protein, SEQ ID 2440.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 8; Length 1049;
Best Local Similarity 18.8%; Pred. No. 2.9e+02;
RESULT 1413
ID ADH82607 standard; protein; 1049 AA.
DE Streptococcus agalactiae protein, SEQ ID 3748.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 8; Length 1049;
Best Local Similarity 18.8%; Pred. No. 2.9e+02;
RESULT 1414
ID ADP07803 standard; protein; 138 AA.
DE Human secreted protein, seq id 286.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 69.5; DB 8; Length 138;
Best Local Similarity 22.0%; Pred. No. 20;
RESULT 1415
ID ADA33664 standard; protein; 198 AA.
DE Acinetobacter baumannii protein #825.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 198;
Best Local Similarity 23.3%; Pred. No. 33;
RESULT 1416
ID ADB09276 standard; protein; 201 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:3216.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 201;
Best Local Similarity 26.0%; Pred. No. 33;
RESULT 1417
ID AEB41646 standard; protein; 201 AA.
DE L. pneumophila protein SEQ ID NO 5978.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.8%; Score 69.5; DB 9; Length 201;
Best Local Similarity 17.6%; Pred. No. 33;
RESULT 1418
ID AAU29449 standard; protein; 210 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #70.
PN WO200168858-A2.
PD 20-SEP-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 69.5; DB 4; Length 210;
Best Local Similarity 20.9%; Pred. No. 35;
RESULT 1419
ID ABG60737 standard; protein; 210 AA.
DE Novel G protein coupled receptor (nGPR-x) #70.
PN US2002058306-A1.
PD 16-MAY-2002.
PA (VOGE/) VOGELI G.
Query Match 5.8%; Score 69.5; DB 5; Length 210;
Best Local Similarity 20.9%; Pred. No. 35;
RESULT 1420
ID AAU01288 standard; protein; 218 AA.
DE Brassica napus fatty acid desaturase, Fad3C, mutant partial sequence.
PN WO200125453-A2.
PD 12-APR-2001.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 5.8%; Score 69.5; DB 4; Length 218;
Best Local Similarity 29.3%; Pred. No. 37;
RESULT 1421
ID ADB09278 standard; protein; 247 AA.

DE Alloiococcus otitis antigenic protein SEQ ID NO:3218.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 247;
Best Local Similarity 26.0%; Pred. No. 44;
RESULT 1422
ID ARG66935 standard; protein; 253 AA.
DE Novel G-protein coupled receptor related protein #12.
PN WO200240539-A2.
PD 23-MAY-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 253;
Best Local Similarity 24.2%; Pred. No. 46;
RESULT 1423
ID ABB62542 standard; protein; 261 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14418.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 69.5; DB 4; Length 261;
Best Local Similarity 27.7%; Pred. No. 48;
RESULT 1424
ID ABO80446 standard; protein; 270 AA.
DE Pseudomonas aeruginosa polypeptide #12621.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 270;
Best Local Similarity 22.1%; Pred. No. 50;
RESULT 1425
ID ADE86076 standard; protein; 296 AA.
DE Streptomyces hygroscopicus ABC transporter.
PN WO2003082909-A1.
PD 09-OCT-2003.
PA (AMHP) WYETH.
Query Match 5.8%; Score 69.5; DB 7; Length 296;
Best Local Similarity 21.0%; Pred. No. 57;
RESULT 1426
ID AAG71524 standard; protein; 308 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1205.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 60;
RESULT 1427
ID ABB44525 standard; protein; 308 AA.
DE Human GPCR3 polypeptide SEQ ID NO 9.
PN WO200174904-A2.
PD 11-OCT-2001.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 60;
RESULT 1428
ID AAU24742 standard; protein; 308 AA.
DE Human olfactory receptor AOLFPR242.
PN WO200168805-A2.
PD 20-SEP-2001.
PA (SENO-) SENOMYX INC.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 60;
RESULT 1429
ID ABP95703 standard; protein; 308 AA.
DE Human GPCR polypeptide SEQ ID NO 216.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 308;
Best Local Similarity 20.9%; Pred. No. 60;
RESULT 1430
ID AAU95729 standard; protein; 308 AA.

DE Human olfactory and pheromone G protein-coupled receptor #216.
 PN WO200224726-A2.
 PD 28-MAR-2002.
 PA (CHEM-) CHEMCOM SA.
 Query Match 5.8%; Score 69.5; DB 5; Length 308;
 Best Local Similarity 20.9%; Pred. No. 60;
 RESULT 1431
 ID AAU85362 standard; protein; 308 AA.
 DE G-coupled olfactory receptor #223.
 PN WO200198526-A2.
 PD 27-DEC-2001.
 PA (SENO-) SENOMYX INC.
 Query Match 5.8%; Score 69.5; DB 5; Length 308;
 Best Local Similarity 20.9%; Pred. No. 60;
 RESULT 1432
 ID ADC86333 standard; protein; 308 AA.
 DE Human GPCR protein SEQ ID NO:786.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 5.8%; Score 69.5; DB 7; Length 308;
 Best Local Similarity 20.9%; Pred. No. 60;
 RESULT 1433
 ID ABW02126 standard; protein; 308 AA.
 DE Human GPCR3 protein.
 PN US2003195335-A1.
 PD 16-OCT-2003.
 PA (GROS/) GROSSE W M.
 PA (SZEK/) SZEXERES E S.
 PA (CASM/) CASMAN S.
 PA (ALSO/) ALSOBROOK J P.
 PA (BURG/) BURGESS C E.
 PA (PADI/) PADIGARU M.
 PA (TAYL/) TAYLOR S.
 PA (TCHE/) TCHERNEV V T.
 PA (SPYT/) SPYTEK K A.
 PA (LILL/) LI L.
 PA (SHEN/) SHENOY S.
 PA (KEKU/) KEKUDA R.
 PA (GANG/) GANGOLLI E A.
 PA (STON/) STONE D J.
 PA (SMIT/) SMITHSON G.
 PA (MACD/) MACDOUGALL J R.
 Query Match 5.8%; Score 69.5; DB 7; Length 308;
 Best Local Similarity 20.9%; Pred. No. 60;
 RESULT 1434
 ID ABR01671 standard; protein; 316 AA.
 DE Human G protein coupled receptor SEQ ID 202.
 PN WO2003000735-A2.
 PD 03-JAN-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.8%; Score 69.5; DB 6; Length 316;
 Best Local Similarity 20.9%; Pred. No. 63;
 RESULT 1435
 ID ADU20551 standard; protein; 317 AA.
 DE A. thaliana At5g67210 homologue.
 PN WO2004092349-A2.
 PD 28-OCT-2004.
 PA (BADI-) BASF PLANT SCI GMBH.
 Query Match 5.8%; Score 69.5; DB 8; Length 317;
 Best Local Similarity 33.7%; Pred. No. 63;
 RESULT 1436
 ID ADU20398 standard; protein; 317 AA.
 DE A. thaliana drought tolerance-associated protein At5g67210.
 PN WO2004092349-A2.
 PD 28-OCT-2004.
 PA (BADI-) BASF PLANT SCI GMBH.
 Query Match 5.8%; Score 69.5; DB 8; Length 317;
 Best Local Similarity 33.7%; Pred. No. 63;
 RESULT 1437
 ID AAY35360 standard; protein; 321 AA.
 DE Chlamydia pneumoniae involved in the virulence process.

PN WO9927105-A2.
 PD 03-JUN-1999.
 PA (GEST-) GENSET.
 Query Match 5.8%; Score 69.5; DB 2; Length 321;
 Best Local Similarity 21.4%; Pred. No. 64;
 RESULT 1438
 ID ADC33485 standard; protein; 321 AA.
 DE Yeast ARV1.
 PN US6566512-B1.
 PD 20-MAY-2003.
 PA (UYCO-) UNIV COLUMBIA NEW YORK.
 Query Match 5.8%; Score 69.5; DB 7; Length 321;
 Best Local Similarity 18.8%; Pred. No. 64;
 RESULT 1439
 ID ADE37749 standard; protein; 321 AA.
 DE Yeast ARV1 (ARE-2 Required for viability).
 PN US2003186879-A1.
 PD 02-OCT-2003.
 PA (UYCO-) UNIV COLUMBIA NEW YORK.
 Query Match 5.8%; Score 69.5; DB 7; Length 321;
 Best Local Similarity 18.8%; Pred. No. 64;
 RESULT 1440
 ID AAU53139 standard; protein; 327 AA.
 DE Propionibacterium acnes immunogenic protein #14035.
 PN WO200181581-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 5.8%; Score 69.5; DB 4; Length 327;
 Best Local Similarity 25.5%; Pred. No. 66;
 RESULT 1441
 ID ABM49658 standard; protein; 327 AA.
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #14334.
 PN WO2003033515-A1.
 PD 24-APR-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 5.8%; Score 69.5; DB 6; Length 327;
 Best Local Similarity 25.5%; Pred. No. 66;
 RESULT 1442
 ID ADH10684 standard; protein; 354 AA.
 DE Rat Sprague-Dawley putative GCR polypeptide.
 PN WO2003104484-A1.
 PD 18-DEC-2003.
 PA (META-) METABOLEX INC.
 Query Match 5.8%; Score 69.5; DB 8; Length 354;
 Best Local Similarity 22.0%; Pred. No. 73;
 RESULT 1443
 ID AAY05489 standard; protein; 382 AA.
 DE Human EDG-2 protein sequence.
 PN WO9919513-A2.
 PD 22-APR-1999.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 Query Match 5.8%; Score 69.5; DB 2; Length 382;
 Best Local Similarity 20.2%; Pred. No. 81;
 RESULT 1444
 ID RAU00302 standard; protein; 382 AA.
 DE LPA receptor-related amino acid sequence #1.
 PN WO200112838-A2.
 PD 22-FEB-2001.
 PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
 Query Match 5.8%; Score 69.5; DB 4; Length 382;
 Best Local Similarity 20.2%; Pred. No. 81;
 RESULT 1445
 ID ABG76099 standard; protein; 382 AA.
 DE Human lysophosphatidic acid (LPA) receptor EDG-1.
 PN US6485922-B1.
 PD 26-NOV-2002.
 PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
 Query Match 5.8%; Score 69.5; DB 6; Length 382;
 Best Local Similarity 20.2%; Pred. No. 81;
 RESULT 1446
 ID ABB47613 standard; protein; 400 AA.
 DE Listeria monocytogenes protein #317.
 PN WO200177335-A2.

PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.8%; Score 69.5; DB 5; Length 400;
Best Local Similarity 22.9%; Pred. No. 87;
RESULT 1447
ID ABU32698 standard; protein; 400 AA.
DE Protein encoded by Prokaryotic essential gene #18225.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 400;
Best Local Similarity 22.9%; Pred. No. 87;
RESULT 1448
ID ADU12060 standard; protein; 401 AA.
DE Drosophila dmt1p1 protein.
PN WO2003002137-A2.
PD 09-JAN-2003.
PA (DRVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 5.8%; Score 69.5; DB 7; Length 401;
Best Local Similarity 20.9%; Pred. No. 87;
RESULT 1449
ID ABB60948 standard; protein; 415 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9636.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 69.5; DB 4; Length 415;
Best Local Similarity 20.9%; Pred. No. 91;
RESULT 1450
ID ADU12059 standard; protein; 415 AA.
DE Drosophila dmt1p1alt2 protein.
PN WO2003002137-A2.
PD 09-JAN-2003.
PA (DRVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 5.8%; Score 69.5; DB 7; Length 415;
Best Local Similarity 20.9%; Pred. No. 91;
RESULT 1451
ID ABB66992 standard; protein; 428 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 27768.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 69.5; DB 4; Length 428;
Best Local Similarity 20.9%; Pred. No. 95;
RESULT 1452
ID ADU12058 standard; protein; 428 AA.
DE Drosophila dmt1p1alt1 protein.
PN WO2003002137-A2.
PD 09-JAN-2003.
PA (DRVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match 5.8%; Score 69.5; DB 7; Length 428;
Best Local Similarity 20.9%; Pred. No. 95;
RESULT 1453
ID AAY41284 standard; protein; 444 AA.
DE CI-NT-his fusion protein encoded by plasmid pLJM6-09.
PN WO9953033-A1.
PD 21-OCT-1999.
PA (UYVA-) UNIV VANDERBILT.
Query Match 5.8%; Score 69.5; DB 2; Length 444;
Best Local Similarity 23.6%; Pred. No. 1e+02;
RESULT 1454
ID AAG30875 standard; protein; 453 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36988.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 3; Length 453;
Best Local Similarity 23.3%; Pred. No. 1e+02;
RESULT 1455
ID ADK47327 standard; protein; 453 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3842.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 5.8%; Score 69.5; DB 8; Length 453;
Best Local Similarity 24.4%; Pred. No. 1e+02;
RESULT 1456
ID ADR95087 standard; protein; 461 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 3722.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 461;
Best Local Similarity 24.4%; Pred. No. 1.1e+02;
RESULT 1457
ID AEA59957 standard; protein; 461 AA.
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:3722.
PN US2005136404-A1.
PD 23-JUN-2005.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 5.8%; Score 69.5; DB 9; Length 461;
Best Local Similarity 24.4%; Pred. No. 1.1e+02;
RESULT 1458
ID AAG30874 standard; protein; 476 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36987.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 3; Length 476;
Best Local Similarity 23.3%; Pred. No. 1.1e+02;
RESULT 1459
ID ADN23349 standard; protein; 477 AA.
DE Bacterial polypeptide #5002.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 69.5; DB 8; Length 477;
Best Local Similarity 23.5%; Pred. No. 1.1e+02;
RESULT 1460
ID ADS28512 standard; protein; 490 AA.
DE Bacterial polypeptide #17545.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 69.5; DB 8; Length 490;
Best Local Similarity 21.2%; Pred. No. 1.1e+02;
RESULT 1461
ID ABO61637 standard; protein; 494 AA.
DE Klebsiella pneumoniae polypeptide seqid 8154.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 494;
Best Local Similarity 22.0%; Pred. No. 1.2e+02;
RESULT 1462
ID AAY41278 standard; protein; 500 AA.
DE Fusion protein containing rabbit prostaglandin E2EP3 receptor.
PN WO9953033-A1.
PD 21-OCT-1999.
PA (UYVA-) UNIV VANDERBILT.
Query Match 5.8%; Score 69.5; DB 2; Length 500;
Best Local Similarity 23.6%; Pred. No. 1.2e+02;
RESULT 1463
ID AAG30873 standard; protein; 503 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36986.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 3; Length 503;
Best Local Similarity 23.3%; Pred. No. 1.2e+02;

RESULT 1454
ID AAY92829 standard; protein; 535 AA.
DE C. pneumoniae CPN100557 processed antigen.
PN WO200024765-A2.
PD 04-MAY-2000.
PA (CONN-) CONNAUGHT LAB LTD.
Query Match 5.8%; Score 69.5; DB 3; Length 535;
Best Local Similarity 21.4%; Pred. No. 1.3e+02;
RESULT 1465
ID ADR13717 standard; protein; 540 AA.
DE Amidase, SEQ ID 54.
PN WO2004069848-A2.
PD 19-AUG-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 540;
Best Local Similarity 23.7%; Pred. No. 1.3e+02;
RESULT 1466
ID AAY92828 standard; protein; 547 AA.
DE C. pneumoniae CPN100557 antigen.
PN WO200024765-A2.
PD 04-MAY-2000.
PA (CONN-) CONNAUGHT LAB LTD.
Query Match 5.8%; Score 69.5; DB 3; Length 547;
Best Local Similarity 21.4%; Pred. No. 1.3e+02;
RESULT 1467
ID ABU26764 standard; protein; 547 AA.
DE Protein encoded by Prokaryotic essential gene #12291.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 547;
Best Local Similarity 21.4%; Pred. No. 1.3e+02;
RESULT 1468
ID ABU31940 standard; protein; 551 AA.
DE Protein encoded by Prokaryotic essential gene #17467.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 551;
Best Local Similarity 23.6%; Pred. No. 1.4e+02;
RESULT 1469
ID AAY01650 standard; protein; 557 AA.
DE A protein with cation transporting activity.
PN WO9913072-A1.
PD 18-MAR-1999.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.8%; Score 69.5; DB 2; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.4e+02;
RESULT 1470
ID AAY83929 standard; protein; 557 AA.
DE Human carnitine transporter protein OCTN2.
PN WO200014210-A1.
PD 16-MAR-2000.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.8%; Score 69.5; DB 3; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.4e+02;
RESULT 1471
ID ABG03029 standard; protein; 557 AA.
DE Novel human diagnostic protein #3020.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 4; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.4e+02;
RESULT 1472
ID ABB82979 standard; protein; 557 AA.
DE Human SLC22A related protein-GenBank Identifier No. GI# 3242598.
PN WO200299053-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 5; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.4e+02;
RESULT 1473
ID ABB82980 standard; protein; 557 AA.
DE Human SLC22A related protein-GenBank Identifier No. GI# 4507005.
PN WO200299053-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.4e+02;
RESULT 1474
ID ABO07242 standard; protein; 557 AA.
DE Human p53 modifying protein, SEQ ID 202.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.4e+02;
RESULT 1475
ID ADE09321 standard; protein; 557 AA.
DE Novel protein-related contig polypeptide sequence #387.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.4e+02;
RESULT 1476
ID ADE09261 standard; protein; 557 AA.
DE Novel protein-related contig polypeptide sequence #327.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.4e+02;
RESULT 1477
ID ADP23817 standard; protein; 557 AA.
DE PRO polypeptide SEQ ID NO:995.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.8%; Score 69.5; DB 8; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.4e+02;
RESULT 1478
ID ADY79867 standard; protein; 557 AA.
DE Amino acid sequence of a human SLC22A5 polypeptide.
PN WO2005026724-A2.
PD 24-MAR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 5.8%; Score 69.5; DB 9; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.4e+02;
RESULT 1479
ID ADA34637 standard; protein; 559 AA.
DE Acinetobacter baumannii protein #1798.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 559;
Best Local Similarity 20.2%; Pred. No. 1.4e+02;
RESULT 1480
ID ABO62908 standard; protein; 564 AA.
DE Klebsiella pneumoniae polypeptide segid 9425.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 564;
Best Local Similarity 23.6%; Pred. No. 1.4e+02;
RESULT 1481
ID ABB89665 standard; protein; 568 AA.
DE Human polypeptide SEQ ID NO 2041.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 69.5; DB 5; Length 568;
Best Local Similarity 22.4%; Pred. No. 1.4e+02;
RESULT 1482
ID ADB65515 standard; protein; 573 AA.

DE Human protein encoded by clone TEST120271790.
FN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 69.5; DB 7; Length 573;
Best Local Similarity 22.7%; Pred. No. 1.4e+02;
RESULT 1483
ID ABP47410 standard; protein; 579 AA.
DE Listeria monocytogenes protein #114.
FN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.8%; Score 69.5; DB 5; Length 579;
Best Local Similarity 21.1%; Pred. No. 1.4e+02;
RESULT 1484
ID ABU32703 standard; protein; 579 AA.
DE Protein encoded by Prokaryotic essential gene #18230.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 579;
Best Local Similarity 21.1%; Pred. No. 1.4e+02;
RESULT 1485
ID ABP65234 standard; protein; 599 AA.
DE Hypoxia-regulated protein #108.
FN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 5.8%; Score 69.5; DB 5; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.5e+02;
RESULT 1486
ID AAE38584 standard; protein; 599 AA.
DE Human GATL GABA transporter protein.
FN WO2003061573-A2.
PD 31-JUL-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 69.5; DB 7; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.5e+02;
RESULT 1487
ID ADD46025 standard; protein; 599 AA.
DE Human Protein P30531, SEQ ID NO 11697.
FN WO2003016475-A2.
PD 27-FEB-2003.
PA (GPHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 69.5; DB 7; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.5e+02;
RESULT 1488
ID AAY41285 standard; protein; 656 AA.
DE CI-77A-TL fusion protein encoded by plasmid pLJM5-42T.
FN WO9953033-A1.
PD 21-OCT-1999.
PA (UTVA-) UNIV VANDERBILT.
Query Match 5.8%; Score 69.5; DB 2; Length 656;
Best Local Similarity 23.6%; Pred. No. 1.7e+02;
RESULT 1489
ID ABP40194 standard; protein; 660 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5039.
FN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 660;
Best Local Similarity 27.2%; Pred. No. 1.7e+02;
RESULT 1490
ID ADS07250 standard; protein; 660 AA.
DE Staphylococcus epidermidis polypeptide seqid 6545.
FN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 5.8%; Score 69.5; DB 8; Length 660;
Best Local Similarity 27.2%; Pred. No. 1.7e+02;

RESULT 1491
ID AAY17390 standard; protein; 663 AA.
DE Human vesicle membrane protein-like protein 3.
FN WO9921994-A2.
PD 06-MAY-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 5.8%; Score 69.5; DB 2; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.7e+02;
RESULT 1492
ID ADM83092 standard; protein; 663 AA.
DE Human vesicle membrane protein (VMP) 2.
FN US2003117587-A1.
PD 18-SEP-2003.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.7e+02;
RESULT 1493
ID ADU64317 standard; protein; 663 AA.
DE Cartilage differentiation inhibiting protein, SEQ ID 12.
FN WO2004013326-A1.
PD 12-FEB-2004.
PA (ASAH) ASAHI KASEI KK.
Query Match 5.8%; Score 69.5; DB 8; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.7e+02;
RESULT 1494
ID ADQ96536 standard; protein; 663 AA.
DE T cell activation associated protein #357.
FN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.7e+02;
RESULT 1495
ID ADY19824 standard; protein; 663 AA.
DE PRO polypeptide SEQ ID NO 5630.
FN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 5.8%; Score 69.5; DB 9; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.7e+02;
RESULT 1496
ID ADY14394 standard; protein; 663 AA.
DE PRO polypeptide SEQ ID NO 200.
FN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 5.8%; Score 69.5; DB 9; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.7e+02;
RESULT 1497
ID ADO09827 standard; protein; 681 AA.
DE Hamster SGLT homologue protein SEQ ID NO:50.
FN WO2004039405-A1.
PD 13-MAY-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69.5; DB 8; Length 681;
Best Local Similarity 24.5%; Pred. No. 1.8e+02;
RESULT 1498
ID ABU41908 standard; protein; 695 AA.
DE Protein encoded by Prokaryotic essential gene #27435.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 695;
Best Local Similarity 24.3%; Pred. No. 1.9e+02;
RESULT 1499
ID ADJ48367 standard; protein; 764 AA.
DE Maize oil-associated gene protein #26.
FN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.

PA (ROGE/) ROGERS J A. 5.8%; Score 69.5; DB 8; Length 764;
Query Match 21.0%; Pred. No. 2.1e+02;
Best Local Similarity 21.0%; Pred. No. 2.1e+02;
RESULT 1500
ID ABU43821 standard; protein; 801 AA.
DE Protein encoded by Prokaryotic essential gene #29348.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. 5.8%; Score 69.5; DB 6; Length 801;
Query Match 19.9%; Pred. No. 2.3e+02;
Best Local Similarity 19.9%; Pred. No. 2.3e+02;

GenCore version 5.1.9
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OM protein - protein search, using sw model
Run on: December 30, 2006, 16:47:16 ; Search time 50 Seconds
(without alignments)
409.643 Million cell updates/sec
Title: US-10-063-519-14
Perfect score: 1195
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 650591 seqs, 87530628 residues
Total number of hits satisfying chosen parameters: 650591
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents AA.*
1: /EMC Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep.*
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3: /EMC Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep.*
4: /EMC Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep.*
6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep.*
7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				* Query Match Length DB ID		Description	
Result No.	Score	Match	Length	DB	ID	Description	
1	669.5	56.0	176	2	US-10-104-047-2567	Sequence 2567, Ap	
2	664	55.6	445	1	US-08-691-814B-6	Sequence 6, Appli	
3	85.5	7.2	449	2	US-09-949-016-8594	Sequence 8594, Ap	
4	82.5	6.9	341	1	US-08-846-762-32	Sequence 92, Appl	
5	80.5	6.7	350	2	US-09-489-039A-9711	Sequence 9711, Ap	
6	80.5	6.7	891	2	US-10-226-629A-16	Sequence 16, Appl	
7	79.5	6.7	406	2	US-09-171-699-4	Sequence 4, Appli	
8	79.5	6.7	406	5	PCT-US94-02107-2	Sequence 2, Appli	
9	79.5	6.7	723	2	US-09-976-594-503	Sequence 503, App	
10	78.5	6.6	221	2	US-09-270-767-41033	Sequence 41033, A	
11	78.5	6.6	221	2	US-09-270-767-56249	Sequence 56249, A	
12	78.5	6.6	766	2	US-09-724-653-2	Sequence 2, Appli	
13	78.5	6.6	766	2	US-09-724-653-14	Sequence 14, Appl	
14	78.5	6.6	766	2	US-09-724-653-15	Sequence 15, Appl	
15	78	6.5	228	2	US-08-248-796A-20444	Sequence 20444, A	
16	78	6.5	251	2	US-09-270-767-43373	Sequence 43373, A	
17	78	6.5	355	2	US-08-833-752-9	Sequence 9, Appli	
18	78	6.5	355	2	US-09-938-719-9	Sequence 9, Appli	
19	78	6.5	355	2	US-09-938-226B-9	Sequence 9, Appli	
20	78	6.5	355	2	US-09-938-703B-9	Sequence 9, Appli	
21	77.5	6.5	892	2	US-10-226-629A-15	Sequence 15, Appl	
22	77	6.4	353	1	US-08-466-103A-14	Sequence 14, Appl	
23	77	6.4	353	2	US-09-280-420-2	Sequence 2, Appli	
24	77	6.4	353	2	US-09-479-195-2	Sequence 2, Appli	
25	76.5	6.4	435	2	US-09-489-039A-12344	Sequence 12344, A	
26	76.5	6.4	494	1	US-08-464-340A-4	Sequence 4, Appli	

27	76.5	6.4	494	5	PCT-US94-08449A-4	Sequence 4, Appli
28	76.5	6.4	555	2	US-10-104-047-2011	Sequence 2011, Ap
29	76	6.4	195	2	US-09-134-000C-5952	Sequence 5952, Ap
30	76	6.4	533	2	US-09-720-317A-22	Sequence 22, Appl
31	75.5	6.3	263	2	US-09-583-110-3148	Sequence 3148, Ap
32	75.5	6.3	263	2	US-09-769-787-119	Sequence 119, App
33	75.5	6.3	264	2	US-09-107-433-4877	Sequence 4877, Ap
34	75.5	6.3	352	2	US-09-492-709A-293	Sequence 293, App
35	75.5	6.3	355	2	US-09-248-796A-14258	Sequence 14258, A
36	75.5	6.3	397	2	US-09-721-870-105	Sequence 105, App
37	75.5	6.3	433	2	US-09-721-870-107	Sequence 107, App
38	75.5	6.3	471	1	US-08-477-451-20	Sequence 20, Appl
39	75.5	6.3	499	2	US-09-721-870-40	Sequence 40, Appl
40	75	6.3	467	2	US-09-328-352-5465	Sequence 5465, Ap
41	75	6.3	549	2	US-09-134-000C-4375	Sequence 4375, Ap
42	75	6.3	1131	2	US-10-104-047-2866	Sequence 2866, Ap
43	74.5	6.2	355	1	US-08-153-848-28	Sequence 28, Appl
44	74.5	6.2	355	1	US-08-153-848-32	Sequence 32, Appl
45	74.5	6.2	355	2	US-09-299-843A-28	Sequence 28, Appl
46	74.5	6.2	355	2	US-09-299-843A-32	Sequence 32, Appl
47	74.5	6.2	355	2	US-09-088-337B-28	Sequence 28, Appl
48	74.5	6.2	355	2	US-09-088-337B-32	Sequence 32, Appl
49	74.5	6.2	355	2	US-09-170-496B-130	Sequence 130, App
50	74.5	6.2	355	2	US-09-170-496B-232	Sequence 232, App
51	74.5	6.2	355	2	US-09-917-254-68	Sequence 68, Appl
52	74.5	6.2	355	5	PCT-US93-11153-38	Sequence 28, Appl
53	74.5	6.2	355	5	PCT-US93-11153-32	Sequence 32, Appl
54	74.5	6.2	471	1	US-07-396-772A-11	Sequence 11, Appl
55	74.5	6.2	471	2	US-09-032-742-2	Sequence 2, Appli
56	74.5	6.2	471	2	US-09-032-742-11	Sequence 11, Appl
57	74.5	6.2	471	2	US-09-032-742-17	Sequence 17, Appl
58	74.5	6.2	471	2	US-09-032-742-14	Sequence 14, Appl
59	74.5	6.2	471	2	US-09-145-864-4	Sequence 4, Appli
60	74.5	6.2	940	2	US-09-328-352-8165	Sequence 8165, Ap
61	74	6.2	154	2	US-09-543-681A-7579	Sequence 7579, Ap
62	74	6.2	332	2	US-09-107-433-2662	Sequence 2662, Ap
63	74	6.2	350	1	US-08-466-103A-12	Sequence 12, Appl
64	74	6.2	353	1	US-08-896-365-6	Sequence 6, Appli
65	74	6.2	680	2	US-09-248-796A-15089	Sequence 15089, A
66	73.5	6.2	312	2	US-09-543-681A-6267	Sequence 6267, Ap
67	73.5	6.2	400	2	US-09-902-540-11488	Sequence 11488, A
68	73.5	6.2	3033	1	US-07-925-695-9	Sequence 9, Appli
69	73	6.1	199	2	US-09-107-532A-6773	Sequence 6773, Ap
70	73	6.1	272	2	US-09-903-456-75	Sequence 75, Appl
71	73	6.1	364	2	US-09-077-675A-16	Sequence 16, Appl
72	73	6.1	364	2	US-09-077-674-16	Sequence 16, Appl
73	73	6.1	364	2	US-09-762-661A-6	Sequence 6, Appli
74	73	6.1	364	2	US-09-743-475-3	Sequence 3, Appli
75	73	6.1	364	2	US-09-743-475-5	Sequence 5, Appli
76	73	6.1	377	2	US-08-936-165A-533	Sequence 533, App
77	73	6.1	494	2	US-09-949-016-7475	Sequence 7475, Ap
78	73	6.1	501	2	US-09-489-039A-9817	Sequence 9817, Ap
79	73	6.1	746	1	US-08-785-431-4	Sequence 4, Appli
80	73	6.1	746	2	US-09-205-048-4	Sequence 4, Appli
81	73	6.1	788	1	US-08-785-431-2	Sequence 2, Appli
82	73	6.1	788	2	US-09-205-048-2	Sequence 2, Appli
83	72.5	6.1	312	2	US-09-248-796A-20385	Sequence 20385, A
84	72.5	6.1	353	2	US-09-134-000C-5562	Sequence 5562, Ap
85	72.5	6.1	359	2	US-09-134-000C-5442	Sequence 5442, Ap
86	72.5	6.1	448	1	US-08-811-897A-16	Sequence 16, Appl
87	72.5	6.1	448	1	US-08-855-213-16	Sequence 16, Appl
88	72.5	6.1	448	2	US-09-201-474-16	Sequence 16, Appl
89	72.5	6.1	476	1	US-08-811-897A-14	Sequence 14, Appl
90	72.5	6.1	476	1	US-08-855-213-14	Sequence 14, Appl
91	72.5	6.1	476	2	US-09-201-474-14	Sequence 14, Appl
92	72.5	6.1	485	1	US-08-811-897A-17	Sequence 17, Appl
93	72.5	6.1	485	2	US-08-855-213-17	Sequence 17, Appl
94	72.5	6.1	485	2	US-09-201-474-17	Sequence 17, Appl
95	72.5	6.1	513	1	US-08-811-897A-15	Sequence 15, Appl
96	72.5	6.1	513	1	US-08-855-213-15	Sequence 15, Appl
97	72.5	6.1	513	2	US-09-201-474-15	Sequence 15, Appl
98	72	6.0	673	2	US-09-949-016-7656	Sequence 7656, Ap
99	72	6.0	696	2	US-09-949-016-6546	Sequence 6546, Ap

100	72	6.0	741	2	US-09-585-858-11	Sequence 11, Appl	173	70.5	5.9	1027	2	US-09-004-225-2	Sequence 2, Appli
101	72	6.0	741	2	US-10-270-878-11	Sequence 11, Appl	174	70.5	5.9	1027	2	US-09-084-346-2	Sequence 2, Appli
102	72	6.0	1038	2	US-09-538-092-487	Sequence 487, App	175	70.5	5.9	1027	2	US-09-104-704-2	Sequence 2, Appli
103	72	6.0	2307	2	US-09-263-933-2	Sequence 2, Appli	176	70.5	5.9	1780	1	US-08-769-309A-5	Sequence 5, Appli
104	72	6.0	2307	2	US-09-263-933-9	Sequence 9, Appli	177	70.5	5.9	1780	2	US-08-994-570-5	Sequence 5, Appli
105	72	6.0	2307	2	US-09-263-933-16	Sequence 16, Appli	178	70.5	5.9	1781	2	US-09-961-403-13	Sequence 13, Appli
106	72	6.0	2307	2	US-09-919-901-2	Sequence 2, Appli	179	70	5.9	142	2	US-09-248-796A-27134	Sequence 27134, A
107	72	6.0	2307	2	US-09-919-901-9	Sequence 9, Appli	180	70	5.9	153	1	US-08-896-365-9	Sequence 9, Appli
108	72	6.0	2307	2	US-09-919-901-16	Sequence 16, Appli	181	70	5.9	298	2	US-09-270-767-34605	Sequence 34605, A
109	72	6.0	2307	2	US-10-191-966-2	Sequence 2, Appli	182	70	5.9	298	2	US-09-270-767-49822	Sequence 49822, A
110	72	6.0	2307	2	US-10-191-966-9	Sequence 9, Appli	183	70	5.9	307	2	US-09-583-110-5003	Sequence 5003, Ap
111	72	6.0	2307	2	US-10-191-966-16	Sequence 16, Appli	184	70	5.9	333	1	US-08-148-215A-4	Sequence 4, Appli
112	71.5	6.0	342	2	US-08-785-928-1	Sequence 1, Appli	185	70	5.9	333	2	US-09-170-496D-16	Sequence 16, Appli
113	71.5	6.0	342	2	US-08-728-603-17	Sequence 17, Appli	186	70	5.9	333	2	US-09-170-496D-172	Sequence 172, App
114	71.5	6.0	366	1	US-08-466-103A-4	Sequence 4, Appli	187	70	5.9	338	2	US-09-248-796A-17918	Sequence 17918, A
115	71.5	6.0	366	1	US-08-896-365-7	Sequence 7, Appli	188	70	5.9	361	2	US-09-270-767-40072	Sequence 40072, A
116	71.5	6.0	382	2	US-09-262-477-2	Sequence 2, Appli	189	70	5.9	361	2	US-09-270-767-55288	Sequence 55288, A
117	71.5	6.0	510	2	US-09-679-686B-19	Sequence 19, Appli	190	70	5.9	399	2	US-09-248-796A-16608	Sequence 16608, A
118	71.5	6.0	670	2	US-09-575-081B-26	Sequence 26, Appli	191	70	5.9	399	2	US-10-094-749-1978	Sequence 1978, Ap
119	71.5	6.0	724	2	US-09-949-016-10086	Sequence 10086, A	192	70	5.9	412	2	US-09-248-796A-22404	Sequence 22404, A
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121	71	5.9	423	5	PCT-US93-08528-38	Sequence 2986, Ap	194	70	5.9	471	2	US-09-328-352-5397	Sequence 5397, Ap
122	71	5.9	423	2	US-09-540-236-29988	Sequence 25, Appli	196	70	5.9	767	2	US-09-328-314-17	Sequence 17, Appli
123	71	5.9	470	2	US-09-292-071-25	Sequence 25, Appli	197	69.5	5.8	198	2	US-09-540-236-2346	Sequence 2346, Ap
124	71	5.9	470	2	US-09-292-069A-25	Sequence 25, Appli	198	69.5	5.8	270	2	US-09-328-352-4951	Sequence 4951, Ap
125	71	5.9	470	2	US-09-292-013-25	Sequence 25, Appli	199	69.5	5.8	321	2	US-09-252-991A-29192	Sequence 29192, A
126	71	5.9	470	2	US-09-292-072-25	Sequence 25, Appli	200	69.5	5.8	321	2	US-09-198-452A-778	Sequence 778, App
127	71	5.9	470	2	US-10-176-255-25	Sequence 25, Appli	201	69.5	5.8	382	2	US-09-688-019-2	Sequence 2, Appli
128	71	5.9	471	1	US-07-817-920-8	Sequence 8, Appli	202	69.5	5.8	453	2	US-09-169-205D-21	Sequence 21, Appli
129	71	5.9	471	1	US-08-370-542-7	Sequence 7, Appli	203	69.5	5.8	461	2	US-09-583-110-3842	Sequence 3842, Ap
130	71	5.9	471	1	US-08-117-006-8	Sequence 8, Appli	204	69.5	5.8	494	2	US-09-107-433-3722	Sequence 3722, Ap
131	71	5.9	471	1	US-08-216-594-8	Sequence 8, Appli	205	69.5	5.8	557	2	US-09-489-039A-8154	Sequence 8154, Ap
132	71	5.9	471	1	US-08-542-358-7	Sequence 7, Appli	206	69.5	5.8	557	2	US-10-327-189-4	Sequence 4, Appli
133	71	5.9	471	1	US-08-244-434-2	Sequence 2, Appli	207	69.5	5.8	557	2	US-09-521-195B-3	Sequence 3, Appli
134	71	5.9	471	2	US-09-018-351-7	Sequence 7, Appli	208	69.5	5.8	557	2	US-09-798-743-1	Sequence 1, Appli
135	71	5.9	471	2	US-09-032-742-8	Sequence 8, Appli	209	69.5	5.8	558	2	US-09-949-016-6309	Sequence 6309, Ap
136	71	5.9	471	2	US-09-145-864-2	Sequence 2, Appli	210	69.5	5.8	558	2	US-09-438-185A-732	Sequence 732, App
137	71	5.9	471	2	US-09-170-496D-122	Sequence 122, App	211	69.5	5.8	559	2	US-09-328-352-5924	Sequence 5924, Ap
138	71	5.9	471	2	US-09-170-496D-228	Sequence 228, App	212	69.5	5.8	564	2	US-09-489-039A-9425	Sequence 9425, Ap
139	71	5.9	471	2	US-10-092-138A-28	Sequence 28, Appli	213	69.5	5.8	573	2	US-10-104-047-3669	Sequence 3669, Ap
140	71	5.9	471	5	US-08-681-219A-28	Sequence 28, Appli	214	69.5	5.8	599	1	US-08-301-722A-5	Sequence 5, Appli
141	71	5.9	471	5	PCT-US93-00149-8	Sequence 8, Appli	215	69.5	5.8	660	2	US-09-949-016-7929	Sequence 7929, Ap
142	71	5.9	727	3	US-10-114-270-190	Sequence 190, App	216	69.5	5.8	663	2	US-09-134-001C-5039	Sequence 5039, Ap
143	71	5.9	2296	1	US-08-286-819A-27	Sequence 27, Appli	217	69.5	5.8	676	2	US-08-959-004-5	Sequence 5, Appli
144	71	5.9	2296	1	US-08-980-357-27	Sequence 27, Appli	218	69.5	5.8	877	2	US-09-165-396-5	Sequence 5, Appli
145	71	5.9	2296	2	US-09-357-375-27	Sequence 27, Appli	219	69.5	5.8	1028	2	US-09-328-352-5749	Sequence 5749, Ap
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147	70.5	5.9	297	2	US-09-328-352-7074	Sequence 7074, Ap	221	69.5	5.8	1684	2	US-08-762-500-25	Sequence 25, Appli
148	70.5	5.9	365	2	US-08-155-005A-8	Sequence 8, Appli	222	69.5	5.8	1704	2	US-08-762-500-75	Sequence 75, Appli
149	70.5	5.9	365	2	US-09-363-783-8	Sequence 8, Appli	223	69.5	5.8	1766	2	US-09-032-438C-120	Sequence 120, App
150	70.5	5.9	365	2	US-09-661-758A-8	Sequence 8, Appli	224	69.5	5.8	1930	2	US-09-949-016-10796	Sequence 10796, A
151	70.5	5.9	367	2	US-09-543-681A-4643	Sequence 4643, Ap	225	69	5.8	193	2	US-08-858-207A-430	Sequence 430, App
152	70.5	5.9	379	1	US-08-118-270-32	Sequence 32, Appli	226	69	5.8	340	2	US-09-248-796A-15237	Sequence 15237, A
153	70.5	5.9	379	5	PCT-US93-08528-32	Sequence 32, Appli	227	69	5.8	370	2	US-08-513-974B-26	Sequence 26, Appli
154	70.5	5.9	388	2	US-08-155-005A-6	Sequence 6, Appli	228	69	5.8	370	2	US-08-513-974B-323	Sequence 323, App
155	70.5	5.9	388	2	US-09-363-783-6	Sequence 6, Appli	229	69	5.8	370	2	US-09-172-353-5	Sequence 5, Appli
156	70.5	5.9	390	2	US-08-155-005A-4	Sequence 4, Appli	230	69	5.8	370	2	US-08-776-971-21	Sequence 21, Appli
157	70.5	5.9	390	2	US-08-155-005A-17	Sequence 17, Appli	231	69	5.8	370	2	US-08-776-971-104	Sequence 104, App
158	70.5	5.9	390	2	US-09-363-783-4	Sequence 4, Appli	232	69	5.8	370	2	US-09-799-955-5	Sequence 5, Appli
159	70.5	5.9	390	2	US-09-363-783-17	Sequence 17, Appli	233	69	5.8	370	2	US-09-461-436B-26	Sequence 26, Appli
160	70.5	5.9	390	2	US-09-661-758A-4	Sequence 4, Appli	234	69	5.8	370	2	US-09-576-290-21	Sequence 21, Appli
161	70.5	5.9	390	2	US-09-661-758A-17	Sequence 17, Appli	235	69	5.8	370	2	US-09-576-290-104	Sequence 104, App
162	70.5	5.9	390	2	US-09-134-001C-5370	Sequence 5370, Ap	236	69	5.8	370	2	US-09-716-147-21	Sequence 21, Appli
163	70.5	5.9	539	2	US-09-291-922-26	Sequence 26, Appli	237	69	5.8	388	2	US-09-716-147-104	Sequence 104, App
164	70.5	5.9	539	1	US-07-879-617A-10	Sequence 10, Appli	238	69	5.8	472	2	US-09-489-039A-8418	Sequence 8418, Ap
165	70.5	5.9	539	1	US-08-295-814B-11	Sequence 11, Appli	239	69	5.8	552	2	US-09-270-767-45540	Sequence 45540, A
166	70.5	5.9	599	1	US-08-240-783B-4	Sequence 4, Appli	240	69	5.8	681	2	US-09-543-681A-5453	Sequence 5453, Ap
167	70.5	5.9	599	1	US-08-753-985-10	Sequence 10, Appli	241	69	5.8	681	2	US-09-248-796A-20857	Sequence 20857, A
168	70.5	5.9	599	2	US-09-084-813-4	Sequence 4, Appli	242	69	5.8	725	2	US-09-248-796A-20849	Sequence 20849, A
169	70.5	5.9	599	2	US-09-343-361-11	Sequence 11, Appli	243	69	5.8	139	2	US-09-270-767-36588	Sequence 36588, A
170	70.5	5.9	599	5	PCT-US92-09662-4	Sequence 4, Appli	244	68.5	5.7	139	2	US-09-270-767-51805	Sequence 51805, A
171	70.5	5.9	1027	1	US-08-551-437-2	Sequence 2, Appli	245	68.5	5.7	139	2		

246	68.5	5.7	178	2	US-09-134-000C-3714	Sequence 3714, Ap	319	68	5.7	355	2	US-09-625-573-5	Sequence 5, Appli
247	68.5	5.7	199	2	US-08-478-316-36	Sequence 36, Appl	320	68	5.7	355	2	US-09-960-547-1	Sequence 1, Appli
248	68.5	5.7	199	2	US-09-019-793A-36	Sequence 36, Appl	321	68	5.7	355	2	PCT-US95-00476-5	Sequence 5, Appli
249	68.5	5.7	200	2	US-09-601-326-36	Sequence 36, Appl	322	68	5.7	373	2	US-09-107-532A-7048	Sequence 7048, Ap
250	68.5	5.7	200	2	US-10-428-826-36	Sequence 36, Appl	323	68	5.7	414	2	US-09-489-039A-10869	Sequence 10869, A
251	68.5	5.7	209	2	US-10-001-887-86	Sequence 86, Appl	324	68	5.7	426	2	US-09-486-192-2	Sequence 2, Appli
252	68.5	5.7	225	2	US-09-543-681A-7698	Sequence 7698, Ap	325	68	5.7	426	2	US-10-328-459A-14	Sequence 14, Appl
253	68.5	5.7	225	1	US-08-896-365-8	Sequence 8, Appli	326	68	5.7	471	2	US-08-492-459-14	Sequence 14, Appl
254	68.5	5.7	237	2	US-09-248-796A-20728	Sequence 20728, A	327	68	5.7	471	2	US-08-423-752-14	Sequence 14, Appl
255	68.5	5.7	377	2	US-09-161-994A-12	Sequence 12, Appl	328	68	5.7	471	2	US-08-716-873-8	Sequence 8, Appli
256	68.5	5.7	377	2	US-09-837-751-34	Sequence 34, Appl	329	68	5.7	471	2	US-08-716-873-28	Sequence 28, Appl
257	68.5	5.7	382	2	US-09-542-733-2	Sequence 2, Appli	330	68	5.7	471	2	US-09-368-431-8	Sequence 8, Appli
258	68.5	5.7	383	1	US-08-196-989B-4	Sequence 4, Appli	331	68	5.7	471	2	US-09-368-431-28	Sequence 28, Appl
259	68.5	5.7	383	1	US-08-760-936-4	Sequence 4, Appli	332	68	5.7	471	2	US-09-414-006-14	Sequence 14, Appl
260	68.5	5.7	383	2	US-09-225-024-4	Sequence 4, Appli	333	68	5.7	471	2	US-09-447-223-14	Sequence 14, Appl
261	68.5	5.7	417	2	US-09-134-000C-5002	Sequence 5002, Ap	334	68	5.7	471	2	US-09-951-217-8	Sequence 8, Appli
262	68.5	5.7	420	1	US-08-466-103A-2	Sequence 2, Appli	335	68	5.7	471	2	US-09-951-217-28	Sequence 28, Appl
263	68.5	5.7	437	2	US-09-328-352-5102	Sequence 5102, Ap	336	68	5.7	471	2	US-09-792-024-88	Sequence 88, Appl
264	68.5	5.7	444	2	US-08-482-746-15	Sequence 15, Appl	337	68	5.7	472	2	US-08-492-459-22	Sequence 22, Appl
265	68.5	5.7	444	2	US-09-580-734-15	Sequence 15, Appl	338	68	5.7	472	2	US-08-423-752-22	Sequence 22, Appl
266	68.5	5.7	444	2	US-08-374-009-15	Sequence 15, Appl	339	68	5.7	472	2	US-08-716-873-36	Sequence 36, Appl
267	68.5	5.7	444	2	US-09-191-724-15	Sequence 15, Appl	340	68	5.7	472	2	US-09-368-431-36	Sequence 36, Appl
268	68.5	5.7	444	2	US-09-631-603-11	Sequence 11, Appl	341	68	5.7	472	2	US-09-414-006-22	Sequence 22, Appl
269	68.5	5.7	448	1	US-08-811-897A-22	Sequence 22, Appl	342	68	5.7	472	2	US-09-447-223-22	Sequence 22, Appl
270	68.5	5.7	448	1	US-08-855-213-22	Sequence 22, Appl	343	68	5.7	472	2	US-09-951-217-36	Sequence 36, Appl
271	68.5	5.7	448	2	US-09-201-474-22	Sequence 22, Appl	344	68	5.7	480	1	US-08-440-103-22	Sequence 22, Appl
272	68.5	5.7	448	2	US-09-631-603-19	Sequence 19, Appl	345	68	5.7	480	1	US-08-440-542-22	Sequence 22, Appl
273	68.5	5.7	468	2	US-09-826-509-553	Sequence 553, App	346	68	5.7	480	1	US-08-231-368-22	Sequence 22, Appl
274	68.5	5.7	475	1	US-08-811-897A-26	Sequence 26, Appl	347	68	5.7	480	1	US-08-440-210-22	Sequence 22, Appl
275	68.5	5.7	475	1	US-08-855-213-26	Sequence 26, Appl	348	68	5.7	480	1	US-09-046-604-22	Sequence 22, Appl
276	68.5	5.7	475	1	US-09-201-474-26	Sequence 26, Appl	349	68	5.7	488	1	US-08-115-365-2	Sequence 2, Appli
277	68.5	5.7	476	1	US-08-811-897A-24	Sequence 24, Appl	350	68	5.7	488	1	US-08-586-897-2	Sequence 2, Appli
278	68.5	5.7	476	1	US-08-811-897A-28	Sequence 28, Appl	351	68	5.7	488	2	US-09-826-509-561	Sequence 561, App
279	68.5	5.7	476	1	US-08-855-213-24	Sequence 24, Appl	352	68	5.7	503	1	US-08-484-840-4	Sequence 4, Appli
280	68.5	5.7	476	1	US-08-855-213-28	Sequence 28, Appl	353	68	5.7	503	1	US-08-483-094-4	Sequence 4, Appli
281	68.5	5.7	476	2	US-09-201-474-24	Sequence 24, Appl	354	68	5.7	727	1	US-08-424-424B-2	Sequence 2, Appli
282	68.5	5.7	476	2	US-09-201-474-28	Sequence 28, Appl	355	68	5.7	727	5	PCT-US94-05363A-2	Sequence 2, Appli
283	68.5	5.7	525	1	US-08-811-897A-23	Sequence 23, Appl	356	68	5.7	859	2	US-09-538-092-206	Sequence 206, App
284	68.5	5.7	525	1	US-08-855-213-23	Sequence 23, Appl	357	68	5.7	908	2	US-08-823-110-1	Sequence 1, Appli
285	68.5	5.7	525	2	US-09-201-474-23	Sequence 23, Appl	358	68	5.7	908	2	US-08-604-298-1	Sequence 1, Appli
286	68.5	5.7	548	2	US-09-149-476-469	Sequence 469, App	359	68	5.7	968	2	US-08-651-999A-7	Sequence 7, Appli
287	68.5	5.7	552	1	US-08-811-897A-27	Sequence 27, Appl	360	68	5.7	968	2	US-09-385-752-7	Sequence 7, Appli
288	68.5	5.7	552	2	US-08-855-213-27	Sequence 27, Appl	361	68	5.7	968	2	US-09-949-016-5914	Sequence 5914, Ap
289	68.5	5.7	552	2	US-09-201-474-27	Sequence 27, Appl	362	68	5.7	987	2	US-09-949-016-10368	Sequence 10368, A
290	68.5	5.7	553	1	US-08-811-897A-25	Sequence 25, Appl	363	68	5.7	2013	1	US-08-324-977-12	Sequence 12, Appl
291	68.5	5.7	553	1	US-08-811-897A-29	Sequence 29, Appl	364	68	5.7	2013	1	US-08-384-616-12	Sequence 12, Appl
292	68.5	5.7	553	1	US-08-855-213-25	Sequence 25, Appl	365	68	5.7	2013	1	US-08-904-686A-12	Sequence 12, Appl
293	68.5	5.7	553	1	US-08-855-213-29	Sequence 29, Appl	366	68	5.7	2013	2	US-09-315-850-12	Sequence 12, Appl
294	68.5	5.7	553	2	US-09-201-474-25	Sequence 25, Appl	367	68	5.7	2620	1	US-08-324-977-32	Sequence 32, Appl
295	68.5	5.7	553	2	US-09-201-474-29	Sequence 29, Appl	368	68	5.7	2620	1	US-08-384-616-32	Sequence 32, Appl
296	68.5	5.7	570	2	US-09-949-016-8907	Sequence 8907, Ap	369	68	5.7	2620	2	US-08-904-686A-32	Sequence 32, Appl
297	68.5	5.7	660	2	US-09-252-991A-29885	Sequence 29885, A	370	68	5.7	2621	1	US-09-315-850-32	Sequence 32, Appl
298	68.5	5.7	738	2	US-09-107-532A-5096	Sequence 5096, Ap	371	68	5.7	2621	1	US-08-324-977-36	Sequence 36, Appl
299	68.5	5.7	762	2	US-09-724-653-7	Sequence 7, Appli	372	68	5.7	2621	1	US-08-384-616-36	Sequence 36, Appl
300	68.5	5.7	1296	2	US-09-462-136-9	Sequence 9, Appli	373	68	5.7	2621	2	US-08-904-686A-36	Sequence 36, Appl
301	68	5.7	188	2	US-09-270-767-36930	Sequence 36930, A	374	68	5.7	2621	2	US-09-315-850-36	Sequence 36, Appl
302	68	5.7	188	2	US-09-270-767-52147	Sequence 52147, A	375	68	5.7	3010	1	US-08-324-977-2	Sequence 2, Appli
303	68	5.7	247	2	US-09-603-208A-152	Sequence 152, App	376	68	5.7	3010	1	US-08-324-977-14	Sequence 14, Appl
304	68	5.7	258	2	US-09-053-197A-7	Sequence 7, Appli	377	68	5.7	3010	1	US-08-384-616-2	Sequence 2, Appli
305	68	5.7	258	2	US-09-653-197A-7	Sequence 7, Appli	378	68	5.7	3010	1	US-08-384-616-14	Sequence 14, Appl
306	68	5.7	309	2	US-09-328-352-6344	Sequence 6344, Ap	379	68	5.7	3010	1	US-08-904-686A-2	Sequence 2, Appli
307	68	5.7	346	2	US-09-585-876-2	Sequence 2, Appli	380	68	5.7	3010	1	US-08-904-686A-14	Sequence 14, Appl
308	68	5.7	346	2	US-09-979-603-2	Sequence 2, Appli	381	68	5.7	3010	2	US-09-315-850-2	Sequence 2, Appli
309	68	5.7	346	2	US-10-314-048A-14	Sequence 14, Appl	382	68	5.7	3010	2	US-09-315-850-14	Sequence 14, Appl
310	68	5.7	346	4	US-10-314-048A-88	Sequence 88, Appl	383	67.5	5.6	210	2	US-09-248-796A-20156	Sequence 20156, A
311	68	5.7	346	4	US-10-313-332A-2	Sequence 2, Appli	384	67.5	5.6	253	2	US-09-540-236-3093	Sequence 3093, Ap
312	68	5.7	355	1	US-08-012-988A-2	Sequence 2, Appli	385	67.5	5.6	306	2	US-09-252-991A-32161	Sequence 32161, A
313	68	5.7	355	1	US-08-450-293A-5	Sequence 5, Appli	386	67.5	5.6	345	2	US-09-979-603-18	Sequence 18, Appl
314	68	5.7	355	2	US-08-446-669-5	Sequence 5, Appli	387	67.5	5.6	350	1	US-08-966-316-16	Sequence 16, Appl
315	68	5.7	355	2	US-09-239-938-1	Sequence 1, Appli	388	67.5	5.6	350	2	US-09-721-908-2	Sequence 2, Appli
316	68	5.7	355	2	US-09-886-319A-14	Sequence 14, Appl	389	67.5	5.6	350	2	US-09-721-341-2	Sequence 2, Appli
317	68	5.7	355	2	US-10-039-659A-13	Sequence 13, Appl	390	67.5	5.6	350	2	US-09-721-495B-2	Sequence 2, Appli
318	68	5.7	355	2	US-09-961-068-1	Sequence 1, Appli	391	67.5	5.6	350	2	US-09-721-341-2	Sequence 2, Appli

538	66.5	5.6	3011	3	US-10-232-643-6	Sequence 6, Appli	611	65	5.4	176	3	US-10-613-106-5	Sequence 5, Appli
539	66.5	5.6	3012	5	PCT-US91-02225-10	Sequence 10, Appl	612	65	5.4	180	2	US-10-002-750-45	Sequence 45, Appl
540	66	5.5	1921	2	US-09-270-767-61535	Sequence 61535, A	613	65	5.4	181	2	US-09-126-640-10	Sequence 10, Appl
541	66	5.5	219	2	US-09-248-796A-15621	Sequence 15621, A	614	65	5.4	181	2	US-09-288-292A-10	Sequence 8, Appli
542	66	5.5	248	2	US-09-258-634-4	Sequence 4, Appli	615	65	5.4	182	2	US-08-826-246-8	Sequence 8, Appli
543	66	5.5	282	2	US-09-107-532A-5717	Sequence 5717, Ap	616	65	5.4	182	2	US-08-944-495-8	Sequence 8, Appli
544	66	5.5	289	2	US-09-134-001C-2917	Sequence 2917, Ap	617	65	5.4	182	2	US-08-925-588-8	Sequence 8, Appli
545	66	5.5	302	2	US-09-107-532A-4973	Sequence 4973, Ap	618	65	5.4	182	2	US-09-372-044-8	Sequence 8, Appli
546	66	5.5	316	2	US-09-328-352-6692	Sequence 6692, Ap	619	65	5.4	182	2	US-08-825-486-8	Sequence 8, Appli
547	66	5.5	318	2	US-09-270-767-45996	Sequence 45996, A	620	65	5.4	182	2	US-08-826-248-8	Sequence 8, Appli
548	66	5.5	370	2	US-09-172-353-7	Sequence 7, Appli	621	65	5.4	193	2	US-09-328-352-6034	Sequence 6034, Ap
549	66	5.5	370	2	US-08-776-971-140	Sequence 140, App	622	65	5.4	223	2	US-10-162-012-9	Sequence 9, Appli
550	66	5.5	370	2	US-09-799-955-7	Sequence 7, Appli	623	65	5.4	272	2	US-09-903-456-79	Sequence 79, Appl
551	66	5.5	370	2	US-09-576-290-140	Sequence 140, App	624	65	5.4	278	2	US-09-949-016-8160	Sequence 8160, Ap
552	66	5.5	370	2	US-09-716-147-140	Sequence 140, App	625	65	5.4	282	2	US-09-107-532A-5538	Sequence 5538, Ap
553	66	5.5	381	1	US-08-845-566-3	Sequence 3, Appli	626	65	5.4	311	2	US-09-252-991A-19489	Sequence 19489, A
554	66	5.5	381	1	US-08-467-948A-28	Sequence 28, Appl	627	65	5.4	322	2	US-09-538-092-506	Sequence 506, App
555	66	5.5	381	1	US-08-852-824-18	Sequence 18, Appl	628	65	5.4	336	2	US-09-095-163-2	Sequence 2, Appli
556	66	5.5	381	2	US-08-467-947A-28	Sequence 28, Appl	629	65	5.4	362	2	US-09-485-648-6	Sequence 6, Appli
557	66	5.5	381	2	US-09-731-030A-17	Sequence 17, Appl	630	65	5.4	362	2	US-09-503-565-6	Sequence 6, Appli
558	66	5.5	381	2	US-09-518-383-18	Sequence 18, Appl	631	65	5.4	362	2	US-09-485-649-6	Sequence 6, Appli
559	66	5.5	381	5	PCT-US96-10618-4	Sequence 4, Appli	632	65	5.4	362	2	US-09-485-650-6	Sequence 6, Appli
560	66	5.5	390	3	US-09-944-049-20	Sequence 20, Appl	633	65	5.4	375	2	US-09-799-978-6	Sequence 6, Appli
561	66	5.5	405	2	US-09-799-978-38	Sequence 38, Appl	634	65	5.4	401	2	US-09-799-978-8	Sequence 8, Appli
562	66	5.5	412	2	US-10-138-701-59	Sequence 59, Appl	635	65	5.4	415	1	US-08-110-286A-2	Sequence 2, Appli
563	66	5.5	412	3	US-09-944-049-22	Sequence 22, Appl	636	65	5.4	415	2	US-08-482-746-2	Sequence 2, Appli
564	66	5.5	433	2	US-09-134-000C-6536	Sequence 6536, Ap	637	65	5.4	415	2	US-09-580-734-2	Sequence 2, Appli
565	66	5.5	447	2	US-09-825-923-2	Sequence 2, Appli	638	65	5.4	415	2	US-08-374-009-2	Sequence 2, Appli
566	66	5.5	447	3	US-10-077-870-2	Sequence 2, Appli	639	65	5.4	415	2	US-09-191-724-2	Sequence 2, Appli
567	66	5.5	450	2	US-09-825-923-4	Sequence 4, Appli	640	65	5.4	415	2	US-09-799-978-2	Sequence 2, Appli
568	66	5.5	450	3	US-10-077-870-4	Sequence 4, Appli	641	65	5.4	415	2	US-09-799-978-4	Sequence 4, Appli
569	66	5.5	582	2	US-09-721-870-179	Sequence 179, App	642	65	5.4	415	2	US-09-799-978-40	Sequence 40, Appl
570	66	5.5	583	2	US-08-270-767-38131	Sequence 38131, A	643	65	5.4	415	2	US-09-826-509-483	Sequence 483, App
571	66	5.5	583	2	US-09-270-767-53348	Sequence 53348, A	644	65	5.4	432	2	US-09-710-279-780	Sequence 780, App
572	66	5.5	1250	2	US-08-938-291A-9	Sequence 9, Appli	645	65	5.4	441	2	US-09-540-236-2016	Sequence 2016, Ap
573	66	5.5	1250	2	US-09-589-619-9	Sequence 9, Appli	646	65	5.4	461	1	US-08-672-814D-2	Sequence 2, Appli
574	65.5	5.5	145	2	US-09-134-000C-3453	Sequence 3453, Ap	647	65	5.4	461	2	US-09-333-696-2	Sequence 2, Appli
575	65.5	5.5	155	2	US-09-134-000C-3721	Sequence 3721, Ap	648	65	5.4	461	2	US-09-282-218A-2	Sequence 2, Appli
576	65.5	5.5	166	2	US-09-134-000C-4279	Sequence 4279, Ap	649	65	5.4	463	2	US-08-612-973-46	Sequence 46, Appl
577	65.5	5.5	210	2	US-09-538-092-121	Sequence 121, App	650	65	5.4	463	2	US-08-927-597-46	Sequence 46, Appl
578	65.5	5.5	210	2	US-09-487-558B-320	Sequence 320, App	651	65	5.4	463	2	US-08-928-757-46	Sequence 46, Appl
579	65.5	5.5	291	2	US-09-252-991A-32938	Sequence 32938, A	652	65	5.4	463	3	US-09-973-025-46	Sequence 46, Appl
580	65.5	5.5	356	2	US-09-107-532A-6286	Sequence 6286, Ap	653	65	5.4	490	2	US-08-612-973-36	Sequence 36, Appl
581	65.5	5.5	369	2	US-09-172-353-6	Sequence 6, Appli	654	65	5.4	490	2	US-08-927-597-36	Sequence 36, Appl
582	65.5	5.5	389	2	US-08-799-955-6	Sequence 6, Appli	655	65	5.4	490	3	US-08-928-757-36	Sequence 36, Appl
583	65.5	5.5	369	2	US-09-170-496D-26	Sequence 26, Appl	656	65	5.4	490	3	US-09-973-025-36	Sequence 36, Appl
584	65.5	5.5	369	2	US-09-170-496D-178	Sequence 178, App	657	65	5.4	491	2	US-09-181-339-7	Sequence 7, Appli
585	65.5	5.5	407	2	US-09-252-991A-21511	Sequence 21511, A	658	65	5.4	516	2	US-09-949-016-11239	Sequence 11239, A
586	65.5	5.5	459	2	US-09-694-519-4	Sequence 4, Appli	659	65	5.4	637	2	US-09-543-681A-5869	Sequence 5869, Ap
587	65.5	5.5	468	2	US-09-252-991A-17314	Sequence 17314, A	660	65	5.4	692	2	US-08-612-973-48	Sequence 48, Appl
588	65.5	5.5	487	2	US-08-583-110-4658	Sequence 4658, Ap	661	65	5.4	692	2	US-08-927-597-48	Sequence 48, Appl
589	65.5	5.5	490	2	US-09-107-433-4640	Sequence 4640, Ap	662	65	5.4	692	2	US-08-928-757-48	Sequence 48, Appl
590	65.5	5.5	492	2	US-09-107-532A-6945	Sequence 6945, Ap	663	65	5.4	692	3	US-09-973-025-48	Sequence 50, Appl
591	65.5	5.5	565	2	US-09-248-796A-15726	Sequence 15726, A	664	65	5.4	809	2	US-08-612-973-50	Sequence 50, Appl
592	65.5	5.5	630	2	US-09-342-647-2	Sequence 2, Appli	665	65	5.4	809	2	US-08-927-597-50	Sequence 50, Appl
593	65.5	5.5	718	2	US-09-657-960-3	Sequence 3, Appli	666	65	5.4	809	3	US-08-928-757-50	Sequence 50, Appl
594	65.5	5.5	860	1	US-08-032-817-4	Sequence 4, Appli	667	65	5.4	809	3	US-09-973-025-50	Sequence 50, Appl
595	65.5	5.5	860	2	US-08-485-128-4	Sequence 4, Appli	668	65	5.4	1033	2	US-09-328-352-5138	Sequence 5138, Ap
596	65.5	5.5	860	2	US-09-804-778A-8	Sequence 8, Appli	669	65	5.4	5069	2	US-10-042-665A-5	Sequence 5, Appli
597	65.5	5.5	860	2	US-09-248-637-4	Sequence 4, Appli	670	64.5	5.4	215	2	US-09-107-532A-3730	Sequence 3730, Ap
598	65.5	5.5	959	2	US-09-248-796A-20776	Sequence 20776, A	671	64.5	5.4	263	1	US-08-565-386-9	Sequence 9, Appli
599	65.5	5.5	1143	2	US-10-104-047-2802	Sequence 2802, Ap	672	64.5	5.4	271	2	US-09-328-352-7066	Sequence 7066, Ap
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601	65.5	5.5	1246	1	US-08-218-265-12	Sequence 12, Appl	674	64.5	5.4	328	2	US-09-489-039A-13216	Sequence 13216, A
602	65.5	5.5	1226	2	US-08-521-872-12	Sequence 12, Appl	675	64.5	5.4	333	2	US-09-107-532A-4886	Sequence 4886, Ap
603	65.5	5.5	1226	2	US-08-590-399-12	Sequence 12, Appl	676	64.5	5.4	344	1	US-08-726-575A-2	Sequence 2, Appli
604	65.5	5.5	1410	1	US-08-470-058-4	Sequence 4, Appli	677	64.5	5.4	346	2	US-09-830-230A-684	Sequence 684, App
605	65.5	5.5	1410	2	US-09-037-188-4	Sequence 4, Appli	678	64.5	5.4	349	2	US-09-134-001C-4519	Sequence 4519, Ap
606	65.5	5.5	1410	2	US-09-285-310-4	Sequence 4, Appli	679	64.5	5.4	373	2	US-09-830-230A-683	Sequence 683, App
607	65.5	5.5	1410	2	US-09-753-385-4	Sequence 4, Appli	680	64.5	5.4	393	2	US-09-270-767-42317	Sequence 42317, A
608	65.5	5.5	1427	2	US-09-487-558B-354	Sequence 354, App	681	64.5	5.4	394	2	US-09-107-433-3892	Sequence 3892, Ap
609	65	5.4	126	2	US-09-107-532A-3813	Sequence 3813, Ap	682	64.5	5.4	398	2	US-09-583-110-4666	Sequence 4666, Ap
610	65	5.4	176	2	US-10-002-750-46	Sequence 46, Appl	683	64.5	5.4	400	2	US-09-826-509-491	Sequence 491, App

684	64.5	5.4	407	2	US-09-328-352-5605	Sequence 5605, Ap	757	64	5.4	431	2	US-09-799-978-20	Sequence 20, Appl
685	64.5	5.4	411	1	US-08-336-031-2	Sequence 2, Appli	758	64	5.4	431	2	US-09-881-401-2	Sequence 2, Appli
686	64.5	5.4	411	1	US-08-902-853-7	Sequence 7, Appli	759	64	5.4	431	2	US-10-821-502-2	Sequence 2, Appli
687	64.5	5.4	411	5	PCT-US95-06725-2	Sequence 2, Appli	760	64	5.4	448	3	US-09-252-991A-23910	Sequence 23910, A
688	64.5	5.4	413	2	US-09-799-978-32	Sequence 32, Appl	761	64	5.4	469	2	US-09-328-352-4250	Sequence 4250, Ap
689	64.5	5.4	418	5	PCT-US94-01321-72	Sequence 72, Appl	762	64	5.4	469	2	US-09-944-049-14	Sequence 14, Appl
690	64.5	5.4	437	2	US-09-353-332-2	Sequence 2, Appli	763	64	5.4	481	3	US-09-062-890-38	Sequence 38, Appl
691	64.5	5.4	444	2	US-10-098-6008-33	Sequence 33, Appl	764	64	5.4	501	2	US-09-902-540-11195	Sequence 11195, A
692	64.5	5.4	446	1	US-07-781-254A-2	Sequence 2, Appli	765	64	5.4	501	2	US-09-583-447A-2	Sequence 2, Appli
693	64.5	5.4	446	1	US-07-781-254A-3	Sequence 3, Appli	766	64	5.4	503	2	US-09-583-447A-4	Sequence 4, Appli
694	64.5	5.4	447	1	US-09-252-991A-20563	Sequence 20563, A	767	64	5.4	504	2	US-09-583-447A-4	Sequence 4, Appli
695	64.5	5.4	448	1	US-08-811-897A-18	Sequence 18, Appl	768	64	5.4	534	2	US-09-710-279-920	Sequence 920, App
696	64.5	5.4	448	1	US-08-855-213-18	Sequence 18, Appl	769	64	5.4	555	2	US-09-543-681A-4582	Sequence 4582, Ap
697	64.5	5.4	448	2	US-09-201-474-18	Sequence 18, Appl	770	64	5.4	586	2	US-09-040-725A-1	Sequence 1, Appli
698	64.5	5.4	464	2	US-09-107-532A-5509	Sequence 5509, Ap	771	64	5.4	686	2	US-09-134-000C-5066	Sequence 5066, Ap
699	64.5	5.4	467	1	US-08-811-897A-19	Sequence 19, Appl	772	64	5.4	757	2	US-09-585-858-23	Sequence 23, Appl
700	64.5	5.4	467	1	US-08-855-213-19	Sequence 19, Appl	773	64	5.4	757	2	US-10-270-878-23	Sequence 23, Appl
701	64.5	5.4	467	2	US-09-201-474-19	Sequence 19, Appl	774	64	5.4	967	1	US-08-188-281B-13	Sequence 13, Appl
702	64.5	5.4	476	1	US-08-811-897A-20	Sequence 20, Appl	775	64	5.4	967	5	PCT-US94-07280-13	Sequence 13, Appl
703	64.5	5.4	476	1	US-08-855-213-20	Sequence 20, Appl	776	64	5.4	967	5	PCT-US95-01087-13	Sequence 13, Appl
704	64.5	5.4	476	2	US-08-855-213-20	Sequence 20, Appl	777	64	5.4	1116	2	US-09-543-681A-4379	Sequence 4379, Ap
705	64.5	5.4	482	2	US-09-107-532A-4512	Sequence 4512, Ap	778	64	5.4	1462	2	US-07-792-600-31	Sequence 31, Appl
706	64.5	5.4	483	2	US-09-134-000C-4234	Sequence 4234, Ap	779	64	5.4	1462	2	US-09-157-021-31	Sequence 31, Appl
707	64.5	5.4	486	2	US-09-291-922-10	Sequence 10, Appl	780	64	5.4	1462	2	US-09-156-842-31	Sequence 31, Appl
708	64.5	5.4	487	2	US-09-949-016-9649	Sequence 9649, Ap	781	64	5.4	1462	2	US-09-591-514-31	Sequence 31, Appl
709	64.5	5.4	494	1	US-09-031-392-5	Sequence 5, Appli	782	64	5.4	1648	5	US-08-188-281B-12	Sequence 12, Appl
710	64.5	5.4	494	2	US-09-299-549-5	Sequence 5, Appli	783	64	5.4	1648	5	PCT-US94-07280-12	Sequence 12, Appl
711	64.5	5.4	494	2	US-09-610-417-5	Sequence 5, Appli	784	64	5.4	2436	5	PCT-US95-01087-12	Sequence 12, Appl
712	64.5	5.4	494	2	US-09-610-417-5	Sequence 5, Appli	785	64	5.4	2436	5	US-08-444-818-75	Sequence 75, Appl
713	64.5	5.4	494	1	US-08-811-897B-5	Sequence 5, Appli	786	64	5.4	2772	2	US-08-444-818B-1	Sequence 89, Appl
714	64.5	5.4	495	1	US-08-855-213-21	Sequence 21, Appl	787	64	5.4	3011	1	US-08-188-281B-1	Sequence 1, Appli
715	64.5	5.4	495	2	US-09-201-474-21	Sequence 21, Appl	788	64	5.4	3011	1	US-08-453-552-1	Sequence 1, Appli
716	64.5	5.4	495	2	US-09-201-474-21	Sequence 21, Appl	789	64	5.4	3011	5	US-08-710-637-1	Sequence 1, Appli
717	64.5	5.4	557	2	US-09-805-6948-16	Sequence 16, Appl	790	64	5.4	3011	5	PCT-US93-00907-1	Sequence 1, Appli
718	64.5	5.4	557	2	US-09-521-195B-27	Sequence 27, Appl	791	64	5.4	3011	5	PCT-US94-07280-1	Sequence 1, Appli
719	64.5	5.4	567	3	US-10-172-527A-7	Sequence 7, Appli	792	63.5	5.3	118	2	PCT-US95-01087-1	Sequence 1, Appli
720	64.5	5.4	567	3	US-11-120-422-7	Sequence 7, Appli	793	63.5	5.3	118	2	US-09-627-376-17	Sequence 17, Appl
721	64.5	5.4	570	2	US-09-248-796A-19123	Sequence 19123, A	794	63.5	5.3	124	2	US-10-047-676B-17	Sequence 17, Appl
722	64.5	5.4	576	2	US-08-948-564-16	Sequence 16, Appl	795	63.5	5.3	124	2	US-09-270-767-34829	Sequence 34829, A
723	64.5	5.4	629	3	US-10-375-010-24	Sequence 24, Appl	796	63.5	5.3	124	2	US-09-270-767-50046	Sequence 50046, A
724	64.5	5.4	747	2	US-09-291-922-2	Sequence 2, Appli	797	63.5	5.3	134	2	US-09-513-999C-6305	Sequence 6305, Ap
725	64.5	5.4	757	2	US-09-585-858-24	Sequence 24, Appl	798	63.5	5.3	209	2	US-09-134-000C-3922	Sequence 3922, Ap
726	64.5	5.4	757	2	US-10-270-878-24	Sequence 24, Appl	799	63.5	5.3	219	2	US-09-270-767-41489	Sequence 41489, A
727	64.5	5.4	795	2	US-09-107-532A-5429	Sequence 5429, Ap	800	63.5	5.3	238	2	US-09-107-433-3974	Sequence 3974, Ap
728	64.5	5.4	2146	2	US-09-949-016-6947	Sequence 6947, Ap	801	63.5	5.3	253	3	US-09-602-787A-8	Sequence 8, Appli
729	64.5	5.4	3033	1	US-07-925-695-8	Sequence 8, Appli	802	63.5	5.3	264	2	US-09-489-039A-9738	Sequence 9738, Ap
730	64	5.4	106	2	US-09-270-767-41157	Sequence 41157, A	803	63.5	5.3	275	1	US-08-118-270-66	Sequence 66, Appl
731	64	5.4	106	2	US-09-270-767-56373	Sequence 56373, A	804	63.5	5.3	275	5	PCT-US93-08528-66	Sequence 66, Appl
732	64	5.4	168	2	US-09-543-681A-6129	Sequence 6129, Ap	805	63.5	5.3	289	1	US-09-134-001C-4667	Sequence 4667, Ap
733	64	5.4	198	2	US-09-248-796A-17465	Sequence 17465, A	806	63.5	5.3	289	1	US-08-781-562-4	Sequence 4, Appli
734	64	5.4	216	2	US-09-270-767-46297	Sequence 46297, A	807	63.5	5.3	308	2	US-09-252-991A-16800	Sequence 16800, A
735	64	5.4	284	2	US-09-270-767-37726	Sequence 37726, A	808	63.5	5.3	337	2	US-09-134-048A-28	Sequence 28, Appl
736	64	5.4	284	2	US-09-270-767-52943	Sequence 52943, A	809	63.5	5.3	342	2	US-09-116-498-4	Sequence 4, Appli
737	64	5.4	285	2	US-09-248-796A-14187	Sequence 14187, A	810	63.5	5.3	342	2	US-09-852-156-6	Sequence 6, Appli
738	64	5.4	296	2	US-09-100-804-12	Sequence 12, Appl	811	63.5	5.3	342	2	US-09-852-156-6	Sequence 6, Appli
739	64	5.4	309	3	US-10-770-127-191	Sequence 191, App	812	63.5	5.3	349	2	US-09-252-991A-24644	Sequence 24644, A
740	64	5.4	325	2	US-09-107-532A-4900	Sequence 4900, Ap	813	63.5	5.3	350	2	US-09-558-002-2	Sequence 2, Appli
741	64	5.4	336	2	US-09-848-294-5	Sequence 5, Appli	814	63.5	5.3	358	2	US-09-270-767-41449	Sequence 41449, A
742	64	5.4	351	2	US-08-688-988-28	Sequence 28, Appl	815	63.5	5.3	365	2	US-09-933-999A-5	Sequence 5, Appli
743	64	5.4	357	2	US-09-489-039A-10505	Sequence 10505, A	816	63.5	5.3	372	1	US-08-202-056-5	Sequence 5, Appli
744	64	5.4	363	2	US-09-248-796A-19011	Sequence 19011, A	817	63.5	5.3	372	1	US-08-076-093A-6	Sequence 6, Appli
745	64	5.4	364	2	US-09-489-039A-12017	Sequence 12017, A	818	63.5	5.3	372	1	US-08-701-265-6	Sequence 6, Appli
746	64	5.4	387	2	US-09-134-001C-4082	Sequence 4082, Ap	819	63.5	5.3	372	1	US-08-284-586-6	Sequence 6, Appli
747	64	5.4	411	1	US-08-381-433A-4	Sequence 4, Appli	820	63.5	5.3	372	1	US-08-803-478-6	Sequence 6, Appli
748	64	5.4	411	2	US-09-981-189B-12	Sequence 12, Appl	821	63.5	5.3	372	1	US-08-803-627A-6	Sequence 6, Appli
749	64	5.4	411	2	US-09-799-978-18	Sequence 18, Appl	822	63.5	5.3	372	1	US-08-801-238-6	Sequence 6, Appli
750	64	5.4	411	2	US-09-881-401-4	Sequence 4, Appli	823	63.5	5.3	372	1	US-08-801-238-6	Sequence 6, Appli
751	64	5.4	411	3	US-10-821-502-4	Sequence 4, Appli	824	63.5	5.3	372	2	US-09-104-296-6	Sequence 6, Appli
752	64	5.4	412	2	US-09-489-039A-8361	Sequence 8361, Ap	825	63.5	5.3	372	2	US-08-982-493-8	Sequence 8, Appli
753	64	5.4	413	2	US-09-491-577-72	Sequence 72, Appl	826	63.5	5.3	372	2	US-09-170-496D-200	Sequence 200, App
754	64	5.4	416	2	US-09-540-236-2393	Sequence 2393, Ap	827	63.5	5.3	372	2	US-09-170-496D-200	Sequence 200, App
755	64	5.4	420	2	US-09-583-447A-6	Sequence 6, Appli	828	63.5	5.3	378	2	US-09-949-016-10255	Sequence 10255, A
756	64	5.4	431	2	US-08-981-189B-13	Sequence 13, Appl	829	63.5	5.3	379	2	US-09-248-796A-14491	Sequence 14491, A

830	63.5	5.3	397	2	US-09-583-110-2946	Sequence 2946, Ap	903	5.3	450	1	US-08-444-734A-8	Sequence 8, Appli
831	63.5	5.3	404	2	US-09-107-433-3747	Sequence 3747, Ap	904	5.3	451	2	US-09-134-001C-4420	Sequence 4420, Ap
832	63.5	5.3	406	2	US-09-252-991A-26429	Sequence 26429, A	905	5.3	489	1	US-09-062-890-34	Sequence 34, Appl
833	63.5	5.3	409	2	US-09-326-203A-23	Sequence 23, Appl	906	5.3	489	1	US-09-062-890-36	Sequence 36, Appl
834	63.5	5.3	416	2	US-09-388-352-4300	Sequence 4300, Ap	907	5.3	508	2	US-10-314-048A-16	Sequence 16, Appl
835	63.5	5.3	428	2	US-09-799-978-36	Sequence 36, Appl	908	5.3	508	2	US-10-314-048A-92	Sequence 92, Appl
836	63.5	5.3	437	2	US-09-949-016-8094	Sequence 8094, Ap	909	5.3	509	1	US-08-890-980-2	Sequence 2, Appli
837	63.5	5.3	446	1	US-08-672-814D-11	Sequence 11, Appl	910	5.3	509	2	US-08-890-979-2	Sequence 2, Appli
838	63.5	5.3	446	2	US-09-333-696-11	Sequence 11, Appl	911	5.3	509	2	US-09-032-894-2	Sequence 2, Appli
839	63.5	5.3	446	2	US-09-282-218A-19	Sequence 19, Appl	912	5.3	509	2	US-09-031-626-2	Sequence 2, Appli
840	63.5	5.3	458	2	US-09-252-991A-20655	Sequence 20655, A	913	5.3	509	2	US-09-054-272-59	Sequence 59, Appl
841	63.5	5.3	474	2	US-09-489-039A-10432	Sequence 10432, A	914	5.3	640	2	US-09-252-991A-27542	Sequence 27542, A
842	63.5	5.3	483	1	US-08-194-338-7	Sequence 7, Appli	915	5.3	692	2	US-09-540-236-3150	Sequence 3150, Ap
843	63.5	5.3	489	2	US-09-991-181-138	Sequence 138, App	916	5.3	729	2	US-09-291-922-29	Sequence 29, Appl
844	63.5	5.3	489	2	US-09-990-444-138	Sequence 138, App	917	5.3	795	2	US-09-252-991A-19085	Sequence 19085, A
845	63.5	5.3	489	2	US-09-997-333-138	Sequence 138, App	918	5.3	822	2	US-08-684-932A-38	Sequence 38, Appl
846	63.5	5.3	489	2	US-09-982-598-138	Sequence 138, App	919	5.3	822	2	US-09-618-304B-2	Sequence 2, Appli
847	63.5	5.3	489	2	US-09-989-735-138	Sequence 138, App	920	5.3	822	2	US-10-314-048A-104	Sequence 104, App
848	63.5	5.3	489	3	US-09-989-726-138	Sequence 138, App	921	5.3	943	1	US-08-469-537A-107	Sequence 107, App
849	63.5	5.3	489	3	US-09-997-514-138	Sequence 138, App	922	5.3	1027	2	US-09-902-540-11750	Sequence 11750, A
850	63.5	5.3	489	3	US-09-989-728-138	Sequence 138, App	923	5.3	1802	2	US-09-322-478-18	Sequence 18, Appl
851	63.5	5.3	489	3	US-09-987-349-138	Sequence 138, App	924	5.3	1802	2	US-09-586-106D-18	Sequence 18, Appl
852	63.5	5.3	489	3	US-09-987-653-138	Sequence 138, App	925	5.3	1802	2	US-10-799-870-18	Sequence 18, Appl
853	63.5	5.3	489	3	US-09-989-293A-138	Sequence 138, App	926	5.3	2985	2	US-10-259-275-40	Sequence 40, Appl
854	63.5	5.3	518	2	US-09-543-681A-4949	Sequence 4949, Ap	927	5.2	80	2	US-09-248-796A-26578	Sequence 26578, A
855	63.5	5.3	568	2	US-09-469-200E-10	Sequence 10, Appl	928	5.2	136	1	US-08-477-451-31	Sequence 31, Appl
856	63.5	5.3	568	2	US-10-011-768B-10	Sequence 10, Appl	929	5.2	136	1	US-09-270-767-40416	Sequence 40416, A
857	63.5	5.3	759	1	US-08-637-759B-89	Sequence 89, Appl	930	5.2	140	2	US-09-270-767-55632	Sequence 55632, A
858	63.5	5.3	759	2	US-08-871-355A-89	Sequence 89, Appl	931	5.2	161	2	US-09-413-814-15	Sequence 15, Appl
859	63.5	5.3	759	2	US-09-201-945-89	Sequence 89, Appl	932	5.2	183	2	US-09-107-532A-1797	Sequence 1797, Ap
860	63.5	5.3	759	2	US-09-714-602-89	Sequence 89, Appl	933	5.2	191	2	US-09-270-767-40648	Sequence 40648, A
861	63.5	5.3	866	2	US-08-651-999A-1	Sequence 1, Appli	934	5.2	191	2	US-09-270-767-55864	Sequence 55864, A
862	63.5	5.3	866	2	US-09-385-752-1	Sequence 1, Appli	935	5.2	197	2	US-09-486-147-40	Sequence 40, Appl
863	63.5	5.3	979	2	US-10-104-047-2446	Sequence 2446, Ap	936	5.2	200	2	US-09-270-767-36009	Sequence 36009, A
864	63.5	5.3	2080	2	US-09-382-552-2	Sequence 2, Appli	937	5.2	200	2	US-09-270-767-51226	Sequence 51226, A
865	63	5.3	147	2	US-09-270-767-45186	Sequence 45186, A	938	5.2	214	2	US-09-710-279-774	Sequence 774, App
866	63	5.3	177	2	US-09-492-308A-20	Sequence 20, Appl	939	5.2	221	2	US-09-248-796A-15088	Sequence 15088, A
867	63	5.3	180	2	US-09-107-532A-5495	Sequence 5495, Ap	940	5.2	252	2	US-09-270-767-45203	Sequence 45203, A
868	63	5.3	197	2	US-09-198-452A-403	Sequence 403, App	941	5.2	255	2	US-09-991-181-287	Sequence 287, App
869	63	5.3	218	2	US-09-134-000C-4489	Sequence 4489, App	942	5.2	255	2	US-09-990-444-287	Sequence 287, App
870	63	5.3	233	2	US-09-134-001C-4013	Sequence 4013, Ap	943	5.2	255	2	US-09-997-333-287	Sequence 287, App
871	63	5.3	240	2	US-09-252-991A-29766	Sequence 29766, A	944	5.2	255	2	US-09-992-598-287	Sequence 287, App
872	63	5.3	245	2	US-09-949-016-11068	Sequence 11068, A	945	5.2	255	2	US-09-989-735-287	Sequence 287, App
873	63	5.3	258	2	US-09-830-807-13	Sequence 13, Appl	946	5.2	255	3	US-09-989-726-287	Sequence 287, App
874	63	5.3	259	2	US-09-261-599B-3	Sequence 3, Appli	947	5.2	255	3	US-09-997-514-287	Sequence 287, App
875	63	5.3	259	2	US-09-456-455A-3	Sequence 3, Appli	948	5.2	255	3	US-09-989-728-287	Sequence 287, App
876	63	5.3	259	2	US-10-080-960-25	Sequence 25, Appl	949	5.2	255	3	US-09-997-349-287	Sequence 287, App
877	63	5.3	264	2	US-09-270-767-41787	Sequence 41787, A	950	5.2	255	3	US-09-997-653-287	Sequence 287, App
878	63	5.3	295	2	US-09-583-110-4171	Sequence 4171, Ap	951	5.2	261	3	US-09-989-293A-287	Sequence 287, App
879	63	5.3	299	2	US-09-107-532A-5499	Sequence 5499, Ap	952	5.2	261	2	US-09-328-352-6619	Sequence 6619, Ap
880	63	5.3	333	2	US-09-134-001C-3246	Sequence 3246, Ap	953	5.2	304	2	US-09-252-991A-22398	Sequence 22398, A
881	63	5.3	359	2	US-08-688-988-32	Sequence 32, Appl	954	5.2	304	2	US-09-107-532A-4681	Sequence 4681, Ap
882	63	5.3	361	1	US-08-390-162-4	Sequence 4, Appli	955	5.2	327	1	US-08-926-724-1	Sequence 1, Appli
883	63	5.3	361	1	US-08-685-945B-4	Sequence 4, Appli	956	5.2	327	2	US-09-949-016-6562	Sequence 6562, Ap
884	63	5.3	365	1	US-08-390-162-2	Sequence 2, Appli	957	5.2	341	2	US-09-252-991A-30051	Sequence 30051, A
885	63	5.3	365	1	US-08-685-945B-2	Sequence 2, Appli	958	5.2	342	2	US-09-134-000C-5123	Sequence 5123, Ap
886	63	5.3	366	2	US-09-107-433-5158	Sequence 2, Appli	959	5.2	343	2	US-09-743-871B-1	Sequence 1, Appli
887	63	5.3	370	2	US-09-172-353-2	Sequence 2, Appli	960	5.2	343	2	US-09-743-871B-5	Sequence 5, Appli
888	63	5.3	370	2	US-09-172-353-3	Sequence 3, Appli	961	5.2	345	2	US-09-543-681A-4410	Sequence 4410, Ap
889	63	5.3	370	2	US-09-799-955-2	Sequence 2, Appli	962	5.2	349	2	US-09-162-524-3	Sequence 3, Appli
890	63	5.3	370	2	US-09-799-955-3	Sequence 3, Appli	963	5.2	349	2	US-09-762-661A-2	Sequence 2, Appli
891	63	5.3	383	2	US-09-710-279-2426	Sequence 2426, Ap	964	5.2	352	2	US-09-829-275-5	Sequence 5, Appli
892	63	5.3	384	2	US-09-134-001C-3437	Sequence 3437, Ap	965	5.2	353	2	US-09-949-016-8077	Sequence 8077, Ap
893	63	5.3	388	2	US-09-940-921B-7	Sequence 7, Appli	966	5.2	362	3	US-09-993-844A-8	Sequence 8, Appli
894	63	5.3	415	2	US-08-482-746-13	Sequence 13, Appl	967	5.2	363	2	US-09-830-807-26	Sequence 26, Appl
895	63	5.3	415	2	US-09-580-734-13	Sequence 13, Appl	968	5.2	383	2	US-09-330-235-8	Sequence 8, Appli
896	63	5.3	415	2	US-08-374-009-13	Sequence 13, Appl	969	5.2	383	5	PCT-US94-01321-2	Sequence 2, Appli
897	63	5.3	415	2	US-09-191-724-13	Sequence 22, Appl	970	5.2	432	2	US-09-489-039A-7223	Sequence 434, App
898	63	5.3	415	2	US-09-799-978-22	Sequence 22, Appl	971	5.2	434	2	US-09-198-452A-434	Sequence 434, App
899	63	5.3	422	2	US-09-625-188-12	Sequence 12, Appl	972	5.2	434	2	US-09-438-185A-417	Sequence 417, App
900	63	5.3	431	1	US-08-381-433A-2	Sequence 2, Appli	973	5.2	439	2	US-09-489-039A-13336	Sequence 13336, A
901	63	5.3	441	2	US-09-489-039A-10091	Sequence 10091, A	974	5.2	441	2	US-09-248-796A-16114	Sequence 16114, A
902	63	5.3	450	1	US-08-194-338-5	Sequence 5, Appli	975	5.2	442	2	US-08-121-446-4	Sequence 4, Appli

976	62.5	5.2	442	2	US-09-520-210-10	Sequence 10, Appl	1049	62	5.2	405	2	US-09-489-039A-7574	Sequence 7574, Ap
977	62.5	5.2	442	2	US-09-826-509-497	Sequence 497, App	1050	62	5.2	407	2	US-09-949-016-11348	Sequence 11348, A
978	62.5	5.2	443	2	US-09-161-994A-3	Sequence 3, Appl	1051	62	5.2	409	2	US-09-583-110-3749	Sequence 3749, Ap
979	62.5	5.2	444	2	US-10-098-600A-36	Sequence 36, Appl	1052	62	5.2	412	2	US-09-134-001C-3949	Sequence 3949, Ap
980	62.5	5.2	452	1	US-08-117-361C-1	Sequence 1, Appl	1053	62	5.2	413	2	US-09-107-433-2887	Sequence 2887, Ap
981	62.5	5.2	452	1	US-09-710-727-1834	Sequence 1834, Ap	1054	62	5.2	414	2	US-09-198-452A-414	Sequence 414, App
982	62.5	5.2	453	2	US-09-489-039A-10468	Sequence 10468, A	1055	62	5.2	414	2	US-09-438-185A-396	Sequence 396, App
983	62.5	5.2	453	2	US-09-769-863-14	Sequence 14, Appl	1056	62	5.2	415	2	US-09-799-978-28	Sequence 28, Appl
984	62.5	5.2	453	2	US-09-489-039A-9027	Sequence 9027, Ap	1057	62	5.2	417	2	US-09-710-279-950	Sequence 950, App
985	62.5	5.2	463	2	US-09-134-001C-3973	Sequence 3973, Ap	1058	62	5.2	432	2	US-09-605-703B-1244	Sequence 1244, Ap
986	62.5	5.2	476	2	US-09-489-039A-13646	Sequence 13646, A	1059	62	5.2	447	2	US-09-388-089B-2	Sequence 2, Appl
987	62.5	5.2	480	2	US-09-489-039A-13045	Sequence 13045, A	1060	62	5.2	473	1	US-08-597-236-13	Sequence 13, Appl
988	62.5	5.2	516	2	US-09-949-002-526	Sequence 526, App	1061	62	5.2	473	1	US-08-746-682A-13	Sequence 13, Appl
989	62.5	5.2	533	2	US-09-769-787-60	Sequence 60, Appl	1062	62	5.2	475	2	US-09-388-089B-12	Sequence 12, Appl
990	62.5	5.2	539	2	US-09-949-016-6363	Sequence 6363, Ap	1063	62	5.2	489	1	US-08-589-893-14	Sequence 14, Appl
991	62.5	5.2	541	2	US-09-158-767-19	Sequence 19, Appl	1064	62	5.2	489	1	US-08-589-893-22	Sequence 22, Appl
992	62.5	5.2	541	2	US-09-158-767-20	Sequence 20, Appl	1065	62	5.2	489	1	US-08-589-893-24	Sequence 24, Appl
993	62.5	5.2	541	2	US-09-713-794-19	Sequence 19, Appl	1066	62	5.2	489	1	US-09-020-991-14	Sequence 14, Appl
994	62.5	5.2	541	2	US-09-713-794-20	Sequence 20, Appl	1067	62	5.2	489	1	US-09-020-991-22	Sequence 22, Appl
995	62.5	5.2	557	1	US-08-424-788-6	Sequence 6, Appl	1068	62	5.2	489	1	US-09-020-991-24	Sequence 24, Appl
996	62.5	5.2	578	1	US-08-424-788-5	Sequence 5, Appl	1069	62	5.2	489	1	US-09-062-890-14	Sequence 14, Appl
997	62.5	5.2	578	1	US-08-110-683-2	Sequence 2, Appl	1070	62	5.2	489	1	US-09-062-890-22	Sequence 22, Appl
998	62.5	5.2	578	1	US-08-683-743-2	Sequence 2, Appl	1071	62	5.2	489	1	US-09-062-890-24	Sequence 24, Appl
999	62.5	5.2	578	1	US-08-477-166-2	Sequence 2, Appl	1072	62	5.2	498	2	US-09-388-089B-11	Sequence 11, Appl
1000	62.5	5.2	578	1	US-08-472-092-2	Sequence 2, Appl	1073	62	5.2	499	2	US-09-673-898-6	Sequence 6, Appl
1001	62.5	5.2	578	2	US-09-439-672-2	Sequence 2, Appl	1074	62	5.2	521	2	US-10-094-749-2671	Sequence 2671, Ap
1002	62.5	5.2	578	2	US-09-949-002-322	Sequence 322, App	1075	62	5.2	550	2	US-09-533-427-14	Sequence 14, Appl
1003	62.5	5.2	578	5	PCT-US93-11638-2	Sequence 2, Appl	1076	62	5.2	550	2	US-09-717-789C-14	Sequence 14, Appl
1004	62.5	5.2	605	2	US-09-328-353-7890	Sequence 7890, Ap	1077	62	5.2	567	2	US-09-560-639-7	Sequence 7, Appl
1005	62.5	5.2	628	2	US-09-107-532A-5288	Sequence 5288, Ap	1078	62	5.2	567	2	US-09-173-151A-24	Sequence 24, Appl
1006	62.5	5.2	669	2	US-09-342-647-18	Sequence 18, Appl	1079	62	5.2	567	2	US-09-032-317-39	Sequence 39, Appl
1007	62.5	5.2	785	2	US-09-134-000C-6690	Sequence 6690, Ap	1080	62	5.2	580	2	US-10-104-047-3215	Sequence 3215, Ap
1008	62.5	5.2	796	2	US-09-270-767-40617	Sequence 40617, A	1081	62	5.2	582	2	US-08-194-560-2	Sequence 2, Appl
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1011	62.5	5.2	1768	2	US-09-489-039A-11704	Sequence 11704, A	1084	62	5.2	610	2	US-09-717-789C-3	Sequence 3, Appl
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1013	62	5.2	112	2	US-09-270-767-59183	Sequence 59183, A	1086	62	5.2	687	2	US-10-104-047-2651	Sequence 2651, Ap
1014	62	5.2	129	2	US-09-673-898-10	Sequence 10, Appl	1087	62	5.2	706	2	US-09-538-092-957	Sequence 957, App
1015	62	5.2	238	2	US-09-605-703B-1246	Sequence 1246, Ap	1088	62	5.2	747	2	US-09-949-016-10040	Sequence 10040, A
1016	62	5.2	250	2	US-09-270-767-43784	Sequence 43784, A	1089	62	5.2	775	2	US-09-305-640-2	Sequence 2, Appl
1017	62	5.2	254	2	US-09-248-796A-22532	Sequence 22532, A	1090	62	5.2	775	2	US-09-948-429C-67	Sequence 67, Appl
1018	62	5.2	272	2	US-09-903-456-76	Sequence 76, Appl	1091	62	5.2	800	2	US-09-248-796A-20101	Sequence 20101, A
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1020	62	5.2	272	2	US-09-903-456-81	Sequence 81, Appl	1093	62	5.2	1186	2	US-09-001-982-6	Sequence 6, Appl
1021	62	5.2	280	2	US-09-902-540-10330	Sequence 10330, A	1094	62	5.2	1186	2	US-09-668-650-6	Sequence 6, Appl
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1024	62	5.2	290	2	US-09-134-001C-4893	Sequence 4893, Ap	1097	61.5	5.1	130	2	US-09-600-430-4	Sequence 4, Appl
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1026	62	5.2	295	2	US-09-903-456-86	Sequence 86, Appl	1099	61.5	5.1	170	2	US-09-710-279-1164	Sequence 1164, Ap
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1028	62	5.2	317	1	US-09-489-039A-9602	Sequence 9602, Ap	1101	61.5	5.1	235	2	US-09-902-540-11995	Sequence 11995, A
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1032	62	5.2	355	1	US-07-759-568-1	Sequence 1, Appl	1105	61.5	5.1	269	2	US-09-489-039A-9180	Sequence 9180, Ap
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1046	62	5.2	384	2	US-09-491-577-16	Sequence 16, Appl	1119	61.5	5.1	353	2	US-09-077-675A-3	Sequence 3, Appl
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1126	61.5	5.1	366	2	US-09-743-742B-7	Sequence 7, Appli	1199	61	5.1	241	2	US-09-489-039A-8397	Sequence 8397, Ap
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1128	61.5	5.1	366	2	US-09-762-661A-7	Sequence 7, Appli	1201	61	5.1	256	2	US-09-150-864A-6	Sequence 6, Appli
1129	61.5	5.1	366	2	US-09-364-425B-45	Sequence 45, Appl	1202	61	5.1	256	2	US-08-012-269A-2	Sequence 2, Appli
1130	61.5	5.1	366	2	US-09-743-475-4	Sequence 4, Appli	1203	61	5.1	256	2	US-09-623-545A-3	Sequence 3, Appli
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1132	61.5	5.1	376	1	US-08-465-976A-3	Sequence 3, Appli	1205	61	5.1	256	5	PCN-US96-03965-2	Sequence 2, Appli
1133	61.5	5.1	376	1	US-08-982-412-3	Sequence 3, Appli	1206	61	5.1	261	2	US-09-134-001C-3485	Sequence 3485, Ap
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1135	61.5	5.1	379	2	US-09-740-035-4	Sequence 4, Appli	1208	61	5.1	272	2	US-09-903-456-78	Sequence 78, Appl
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1139	61.5	5.1	391	1	US-08-103-445-5	Sequence 5, Appli	1212	61	5.1	285	2	US-09-543-681A-7666	Sequence 7666, Ap
1140	61.5	5.1	391	1	US-08-461-690B-5	Sequence 5, Appli	1213	61	5.1	285	2	US-09-540-236-2583	Sequence 2583, Ap
1141	61.5	5.1	391	1	US-08-501-003A-16	Sequence 16, Appl	1214	61	5.1	298	2	US-09-438-185A-545	Sequence 545, App
1142	61.5	5.1	391	2	US-09-275-252A-13	Sequence 13, Appl	1215	61	5.1	299	3	US-10-770-127-187	Sequence 187, App
1143	61.5	5.1	392	2	US-09-489-039A-8713	Sequence 8713, Ap	1216	61	5.1	302	2	US-08-311-731A-173	Sequence 173, App
1144	61.5	5.1	397	2	US-09-491-577-32	Sequence 32, Appl	1217	61	5.1	338	2	US-09-107-532A-6222	Sequence 6222, Ap
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1146	61.5	5.1	411	1	US-10-094-749-1666	Sequence 1666, Ap	1219	61	5.1	345	2	US-09-489-039A-7417	Sequence 7417, Ap
1147	61.5	5.1	415	1	US-08-110-286A-6	Sequence 6, Appli	1220	61	5.1	355	2	US-08-833-752-8	Sequence 8, Appli
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1150	61.5	5.1	415	2	US-09-580-734-6	Sequence 6, Appli	1223	61	5.1	355	2	US-09-938-703B-8	Sequence 8, Appli
1151	61.5	5.1	415	2	US-08-374-009-6	Sequence 6, Appli	1224	61	5.1	358	2	US-09-248-796A-19081	Sequence 19081, A
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1158	61.5	5.1	469	2	US-08-956-1718-5245	Sequence 5245, Ap	1231	61	5.1	489	2	US-09-710-279-2632	Sequence 2632, Ap
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1161	61.5	5.1	497	1	US-08-295-670-6	Sequence 6, Appli	1234	61	5.1	545	2	US-09-949-016-6469	Sequence 6469, Ap
1162	61.5	5.1	497	1	US-08-633-485-6	Sequence 6, Appli	1235	61	5.1	558	2	US-09-949-016-7736	Sequence 7736, Ap
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1164	61.5	5.1	524	1	US-09-134-001C-3368	Sequence 3368, Ap	1237	61	5.1	672	2	US-09-556-916-28	Sequence 28, Appl
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1166	61.5	5.1	526	1	US-08-298-426-4	Sequence 4, Appli	1239	61	5.1	724	2	US-09-252-991A-30228	Sequence 30228, A
1167	61.5	5.1	615	2	US-09-602-787A-534	Sequence 534, App	1240	61	5.1	732	2	US-10-160-748-6	Sequence 6, Appli
1168	61.5	5.1	615	2	US-09-602-787A-536	Sequence 536, App	1241	61	5.1	732	2	US-09-248-796A-14319	Sequence 14319, A
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1171	61.5	5.1	685	2	US-09-720-317A-31	Sequence 31, Appl	1244	61	5.1	806	2	US-09-833-466-13	Sequence 13, Appl
1172	61.5	5.1	682	2	US-09-248-796A-18612	Sequence 18612, A	1245	61	5.1	815	2	US-09-107-433-5059	Sequence 5059, Ap
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1179	61.5	5.1	1025	2	US-09-543-681A-7112	Sequence 7112, Ap	1252	61	5.1	1303	2	US-09-600-087-2	Sequence 2, Appli
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1182	61.5	5.1	2247	2	US-09-091-219-2	Sequence 2, Appli	1255	61	5.1	2079	2	US-09-949-016-8301	Sequence 8301, Ap
1183	61.5	5.1	2247	2	US-09-660-541-2	Sequence 2, Appli	1256	61	5.1	2864	2	US-08-469-260A-394	Sequence 394, App
1184	61.5	5.1	3066	2	US-08-922-127-12	Sequence 12, Appl	1257	61	5.1	2864	2	US-08-488-446-394	Sequence 394, App
1185	61	5.1	95	2	US-09-248-796A-21665	Sequence 21665, A	1258	61	5.1	2864	2	US-08-467-344A-394	Sequence 394, App
1186	61	5.1	122	2	US-09-710-279-102	Sequence 102, Appl	1259	61	5.1	2864	2	US-08-424-550B-394	Sequence 394, App
1187	61	5.1	175	1	US-08-408-095-11	Sequence 11, Appl	1260	61	5.1	3011	2	US-08-811-566-20	Sequence 20, Appl
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1189	61	5.1	189	2	US-09-080-643-4	Sequence 4, Appli	1262	61	5.1	3011	2	US-09-034-756-20	Sequence 20, Appl
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1191	61	5.1	200	2	US-09-710-279-1242	Sequence 1242, Ap	1264	61	5.1	3011	2	US-09-952-572-9	Sequence 9, Appli
1192	61	5.1	202	2	US-08-657-749D-17	Sequence 17, Appl	1265	61	5.1	3011	2	US-09-929-955-1	Sequence 1, Appli
1193	61	5.1	206	2	US-09-134-001C-3929	Sequence 3929, Ap	1266	61	5.1	3011	2	US-10-259-275-20	Sequence 20, Appl
1194	61	5.1	207	2	US-08-559-397A-13	Sequence 13, Appl	1267	61	5.1	3011	3	US-10-184-150-3	Sequence 3, Appli

1268	61	5.1	3012	2	US-08-811-566-2	Sequence 2, Appli	1341	60.5	5.1	503	2	US-09-068-195-24	Sequence 24, Appli
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1270	60.5	5.1	73	2	US-09-543-681A-6595	Sequence 6595, Ap	1343	60.5	5.1	512	2	US-09-724-224-4	Sequence 4, Appli
1271	60.5	5.1	107	2	US-09-107-532A-5805	Sequence 5805, Ap	1344	60.5	5.1	512	2	US-10-093-317-4	Sequence 4, Appli
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ALIGNMENTS

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; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2567
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2567
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; Patent No. 5981218
; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Tomasetto, Paul
; APPLICANT: Bassett, Paul
; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, NW, Suite 600
; CITY: Washington
; STATE: DC
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; ZIP: 20005-3934
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,814B
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,183
; FILING DATE: 09-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1383.0090001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 6:
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; MOLECULE TYPE: protein
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; Sequence 8594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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; PRIOR FILING DATE: 2000-09-08
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US-09-489-039A-9711

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; Sequence 16, Application US/10226629A
; Patent No. 6960431
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 891
; TYPE: PRT
; ORGANISM: Vaccinia virus
US-10-226-629A-16

Query Match
Best Local Similarity 6.7%; Score 80.5; DB 2; Length 891;
Matches 38; Conservative 36; Mismatches 70; Indels 19; Gaps 7;

QY 7 DMENALTCGSSSHASLRNIHSINPTQLMAR-IESYEGREKKGISDVRTFCLFVTFDLFF 65
Db 717 NMTNEIT--DMINASLKNITISKNNMLVSQLNSVANRSKQKIGDLRQSSCKMALLPKNL 774
QY 66 VTIILWIELNVNGGIENTLEKVMQ-YDYY-----SSYFDIFLLAVFRPKVILAVACR 119
Db 775 ATSIYTIERFNKVGDDVKASMLEKVKYFTDIDMSLYKOLIAENKAMLYIRRGCR 834
QY 120 LRHWMAIALTT--AVTSAFLAKVILSKL-----FSQAFGYV 155
Db 835 IDD---AQITDDLVKYSYLRPKILSLMNVNYSRGEFHM 874

RESULT 7
US-09-171-699-4
; Sequence 4, Application US/09171699
; Patent No. 6448389
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of, Anatomy & Biology
; APPLICANT: Gonzol, Eva
; APPLICANT: Berencsi, Klara
; APPLICANT: Kari, Ceaba
; TITLE OF INVENTION: No. 6448389el Cytomegalovirus DNA Constructs and Uses Therefor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, P.O. Box 457
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; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,699
; FILING DATE: 19-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/015,717
; FILING DATE: 23-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST66APCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-171-699-4

Query Match
Best Local Similarity 6.7%; Score 79.5; DB 2; Length 406;
Matches 52; Conservative 36; Mismatches 67; Indels 115; Gaps 12;

QY 14 GSOSHASLRNIHSINPTQLMARIESY-----EGREKKGISDVRTFCLFVTFDLFFVTL 68
Db 142 GCSQMAALQNLPCQSPDEIMAYAKIFKILDERDK-----VLTHIDHIFMDI 190
QY 69 LWTIELNVNGGIENTLEKVMQDY-----YSSYFDIFLLAVFRPKVILAVACRL 120
Db 191 L-----ITTCVETMCNEYKVTSDACMTMYGGISLSEF-----CRV 226
QY 121 RHWMAIALTTAVTSAFLAK-----VILSKLFSQAFGYV----- 156
Db 227 LSCYVLEETSV-----MLAKRPLITKPEVISVMKRRIEICMKVFAQ-----YILGADPLR 277
QY 157 ---PIISFILAWIETWFLDPKVLQPEABEENRLLIVQDASERAALIPGGLSDGQFYSPPE 213
Db 278 VCSPSVD-----DLRAIAESDEEAAIVATLATR-----GASSSDSLVSPPE 320
QY 214 S-----EAGSEAEKODSEK 229
Db 321 SPVPATIPLSVVIVAENSQERSEQSDDEE 350

RESULT 8
PCT-US94-02107-2
; Sequence 2, Application PC/TUS9402107
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of, Anatomy and Biology
; TITLE OF INVENTION: Recombinant Cytomegalovirus Vaccine
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: PCT/US94/02107
  FILING DATE:
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/017,130
    FILING DATE: 12-FEB-1993
    ATTORNEY/AGENT INFORMATION:
      NAME: Bak, Mary E.
      REGISTRATION NUMBER: 31,215
      REFERENCE/DOCKET NUMBER: W576BPCT
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: 215-540-9200
        TELEFAX: 215-540-5818
  INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 406 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
PCT-US94-02107-2

Query Match      6.7%; Score 79.5; DB 5; Length 406;
Best Local Similarity 19.3%; Pred. No. 2.1;
Matches 52; Conservative 36; Mismatches 67; Indels 115; Gaps 12;

QY 14 GQSSHASLRNTHSINPTOLMARIESY-----EGREKGISDVRRFTCLFVTFFDLLFVTL 68
Db 142 GCSQMAALQNLPPQCSPEIMAYAQKIFKILDEERDK-----VLTHIDHIFMDI 190
QY 69 LWTIELNVNGGIENTLEKEVMQYDY-----YSSYDFIFLAVPRFKVLILAVAVCRLL 120
Db 191 L-----TTCVETMCNEYKVTSDACMTMYGGSILSEF-----CRV 226
QY 121 RHWMAIALTTAVTSFALAK-----VLSKLFQSGAGYVL----- 156
Db 227 LSCVLEETSV-----MLAKRPLITKPEVISVMKRRIEICMKVFAQ-----YILGADPLR 277
QY 157 ---PIISFILAMETWFLDFKVLPOEAEENRLLIVQDASERAALIPGSLSDGQFYSPPE 213
Db 278 VCSPSVD-----DLRAIAEESDEEAIVAYTLATR-----GASSDSLSVSPPE 320
QY 214 S-----EAGSEAEKQDSEK 229
Db 321 SPVPATIPSSVIVAENSQDESEQSDSEE 350

RESULT 9
US-09-976-594-503
; Sequence 503, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 503
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2246292CD1
US-09-976-594-503
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Query Match      6.7%; Score 79.5; DB 2; Length 723;
Best Local Similarity 18.0%; Pred. No. 4.8;
Matches 34; Conservative 40; Mismatches 58; Indels 57; Gaps 8;

QY 58 FVTFDILLFVTLWIELNVNGGIENTLEKEVMQYDYSSYDFIFLAVPRFKVLI----- 112
Db 13 FMSVDICVTTAIYVF-----SHLDRLSLEDIRHFNFDVLDLWAACLYRSCLLGATIG 67
QY 113 ----LAYAVCRRLR-HWMAIALTTAVTSFALAKVILSKLFQSGQ-----GAGFY 154
Db 68 VAKNSALGPRRLRASLWLVISLCLFVGIIYAMVKLL---LFSEVRRPIRDPNFWALFVWTY 124
QY 155 VLPISFILAMETWFLDFKVLPOEAEENRLLIVQDASERAALIPGSLSDGQFY----- 209
Db 125 ISLGASFLMWL-----LSTVRPGTQ--ALEPFGAATEAGFPFGSGR 163
QY 210 SPPESEAGS 218
Db 164 PPPEQASGA 172
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RESULT 10
US-09-270-767-41033
; Sequence 41033, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41033
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41033
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Query Match      6.6%; Score 78.5; DB 2; Length 221;
Best Local Similarity 22.5%; Pred. No. 1.2;
Matches 38; Conservative 33; Mismatches 73; Indels 25; Gaps 7;

QY 56 CLFVTFDL---LFVTLWIELNVNGGIENTLEKEVMQYDYSSYDFIFLAVPRFKVLI 112
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QY 113 LAYAVCRRLRHWMAIALTT--AVTSFALAKVILSKLFQSGAGYVL--PIISFILAMETW 169
Db 77 VVYFCCSFCTTYQLIQGTVNSINFRNLKNSLT-----LGFLISPPISIHFSYLPY 129
QY 170 FLDFKVLPOEAEENRLL-----IVQDASERAAL--IPGSLSDGQF 208
Db 130 LVNNSVLHLKNVXIQEFLDXVVKCFFFILRASFRFLCKDIPNGL--GQF 176
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RESULT 11
US-09-270-767-56249
; Sequence 56249, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56249
; LENGTH: 221
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; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-720-767-56249

Query Match 6.6%; Score 78.5; DB 2; Length 221;
Best Local Similarity 22.5%; Pred. No. 1.2;
Matches 38; Conservative 33; Mismatches 73; Indels 25; Gaps 7;

QY 56 CLFVTPDL----LFTLLWIIELNVNGGIENTLEKEVMQDYSSYFDIFLLAVFRFKVLI 112

Db 17 CIIYSSMDQFLFIILLILLCLSFVEXYLFVNILXIDNYIGNKNVFLFFLLFOXII 76

QY 113 LAYAVCLRHHWAIALTT--AVTSAPLLAKVILSKLFSQAGFVVL--PIISFILAWIETW 169

Db 77 VVFCCSFCTYQIQTYNSINFRNLKNSLT-----LGLISPPISIHPSYLPHY 129

QY 170 FLDPKVLPOBAEENRLL-----IVQDASERAAL--IPGGLSDGQF 208

Db 130 LVANSVLHLKXVQIEFLDXVKCFPFILRASFRCLKIDPNGL--GQF 176

RESULT 12

US-09-724-653-2
; Sequence 2, Application US/09724653
; Patent No. 6830913

; GENERAL INFORMATION:
; APPLICANT: Ling, Victor

; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: APZ-004CP

; CURRENT APPLICATION NUMBER: US/09/724,653
; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29

; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2

; LENGTH: 766

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-653-2

Query Match 6.6%; Score 78.5; DB 2; Length 766;
Best Local Similarity 18.0%; Pred. No. 6.7;
Matches 34; Conservative 39; Mismatches 59; Indels 57; Gaps 8;

QY 58 FVTFDLLFVTLWIIELNVNGGIENTLEKEVMQDYSSYFDIFLLAVFRFKVLI----- 112

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QY 113 ----LAVAVCLRHHWAIALTTAVTSAPLLAKVILSKLFSQ-----GAFGY 154

Db 68 VAKNSALGPRRLRASMLVITLCLFVGIVAMVKLL---LFSEVRRPIRDPWFALFWWTY 124

QY 155 VLPPIISFILAWIETWFLDPKVLPOBAEENRLLIVQDASERAALIPGGLSDGQFY----- 209

Db 125 ISLGASFLWL-----LSTVRPGTQ--ALEPGAATEABGFPQSGR 163

QY 210 SPPESEAGS 218

Db 164 PPEQASGA 172

RESULT 13

US-09-724-653-14
; Sequence 14, Application US/09724653
; Patent No. 6830913

; GENERAL INFORMATION:
; APPLICANT: Ling, Victor

; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: APZ-004CP

; CURRENT APPLICATION NUMBER: US/09/724,653

; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14

; LENGTH: 766

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-653-14

Query Match 6.6%; Score 78.5; DB 2; Length 766;
Best Local Similarity 18.0%; Pred. No. 6.7;
Matches 34; Conservative 39; Mismatches 59; Indels 57; Gaps 8;

QY 58 FVTFDLLFVTLWIIELNVNGGIENTLEKEVMQDYSSYFDIFLLAVFRFKVLI----- 112

Db 13 FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAAACLYRSCLLGATIG 67

QY 113 ----LAVAVCLRHHWAIALTTAVTSAPLLAKVILSKLFSQ-----GAFGY 154

Db 68 VAKNSALGPRRLRASMLVITLCLFVGIVAMVKLL---LFSEVRRPIRDPWFALFWWTY 124

QY 155 VLPPIISFILAWIETWFLDPKVLPOBAEENRLLIVQDASERAALIPGGLSDGQFY----- 209

Db 125 ISLGASFLWL-----LSTVRPGTQ--ALEPGAATEABGFPQSGR 163

QY 210 SPPESEAGS 218

Db 164 PPEQASGA 172

RESULT 14

US-09-724-653-15

; Sequence 15, Application US/09724653
; Patent No. 6830913

; GENERAL INFORMATION:
; APPLICANT: Ling, Victor

; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: APZ-004CP

; CURRENT APPLICATION NUMBER: US/09/724,653
; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29

; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15

; LENGTH: 766

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-653-15

Query Match 6.6%; Score 78.5; DB 2; Length 766;
Best Local Similarity 18.0%; Pred. No. 6.7;
Matches 34; Conservative 39; Mismatches 59; Indels 57; Gaps 8;

QY 58 FVTFDLLFVTLWIIELNVNGGIENTLEKEVMQDYSSYFDIFLLAVFRFKVLI----- 112

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QY 113 ----LAVAVCLRHHWAIALTTAVTSAPLLAKVILSKLFSQ-----GAFGY 154

Db 68 VAKNSALGPRRLRASMLVITLCLFVGIVAMVKLL---LFSEVRRPIRDPWFALFWWTY 124

QY 155 VLPPIISFILAWIETWFLDPKVLPOBAEENRLLIVQDASERAALIPGGLSDGQFY----- 209

Db 125 ISLGASFLWL-----LSTVRPGTQ--ALEPGAATEABGFPQSGR 163

QY 210 SPPESEAGS 218

Db 164 PPEQASGA 172


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Listing first 1500 summaries

Database : Published Applications AA Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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449 1195 100.0 234 4 US-10-223-085-62 Sequence 62, Appl
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562 1195 100.0 234 4 US-10-063-742-14 Sequence 14, Appl
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670 1195 100.0 234 4 US-10-305-654-62 Sequence 62, Appl
675 1195 100.0 234 4 US-10-081-056-62 Sequence 62, Appl
681 1195 100.0 234 5 US-10-491-566-20 Sequence 20, Appl
682 1195 100.0 234 5 US-10-972-317-14 Sequence 14, Appl
683 1195 100.0 234 5 US-10-485-555-36 Sequence 16, Appl
692 1195 100.0 234 6 US-11-102-240-14 Sequence 14, Appl
693 1195 100.0 234 6 US-11-103-195-14 Sequence 14, Appl
694 1188 99.4 234 4 US-10-262-839-84 Sequence 84, Appl
695 1024 85.7 201 4 US-10-264-237-2663 Sequence 2663, Ap
696 985 82.4 198 4 US-10-262-839-82 Sequence 82, Appl
697 669.5 56.0 176 4 US-10-104-047-2567 Sequence 2567, Ap
698 669.5 56.0 176 6 US-11-072-512-2567 Sequence 2567, Ap
699 664 55.6 445 4 US-10-177-293-296 Sequence 296, Ap
700 664 55.6 445 4 US-10-435-696-33 Sequence 33, Appl
701 625 52.3 534 5 US-10-450-763-35857 Sequence 35857, A
702 578 48.4 412 5 US-10-491-213-22 Sequence 22, Appl

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580 28.7 343 703 6 US-11-097-143-6696 Sequence 6696, Ap
373 7.6 91 704 4 US-10-091-007-198 Sequence 198, App
803 7.6 90.5 705 4 US-10-437-963-136814 Sequence 136814,
516 7.3 87.5 706 3 US-09-925-298-653 Sequence 653, App
516 7.3 87.5 707 3 US-10-102-808-653 Sequence 653, App
421 7.3 87 708 5 US-10-741-600-929 Sequence 929, App
223 7.2 85.5 709 5 US-10-741-600-926 Sequence 926, App
285 7.2 85.5 710 5 US-10-741-600-921 Sequence 921, App
315 7.2 85.5 711 5 US-10-741-600-925 Sequence 925, App
323 7.2 85.5 712 5 US-10-741-600-923 Sequence 923, App
328 7.2 85.5 713 5 US-10-741-600-924 Sequence 924, App
338 7.2 85.5 714 5 US-10-741-600-928 Sequence 928, App
339 7.2 85.5 715 5 US-10-741-600-930 Sequence 930, App
384 7.2 85.5 716 5 US-10-741-600-932 Sequence 932, App
390 7.2 85.5 717 5 US-10-741-600-927 Sequence 927, App
396 7.2 85.5 718 4 US-10-282-122A-54604 Sequence 54604, A
396 7.2 85.5 719 6 US-11-188-298-4394 Sequence 4394, Ap
438 7.2 85.5 720 5 US-10-741-600-931 Sequence 931, App
440 7.2 85.5 721 4 US-10-262-511-182 Sequence 182, App
449 7.2 85.5 722 5 US-10-821-234-1075 Sequence 1075, Ap
473 7.2 85.5 723 4 US-10-264-237-2016 Sequence 2016, Ap
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500 7.2 85.5 725 4 US-10-282-122A-68468 Sequence 68468, A
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102 7.1 84.5 731 4 US-10-282-122A-61134 Sequence 61134, A
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239 7.1 84.5 735 4 US-10-282-122A-63532 Sequence 63532, A
341 6.9 82.5 736 4 US-10-216-209-92 Sequence 92, Appl
389 6.9 82.5 737 5 US-10-831-070-126 Sequence 126, App
589 6.9 82 738 4 US-10-205-194-144 Sequence 144, App
1466 6.9 82 739 5 US-10-732-923-1543 Sequence 1543, Ap
264 6.8 81.5 740 4 US-10-425-114-44166 Sequence 44166, A
436 6.8 81.5 741 4 US-10-424-599-272132 Sequence 272132,
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209 6.7 80 752 4 US-10-425-115-258202 Sequence 258202,
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323 6.6 79 768 5 US-10-732-923-18557 Sequence 18557, A
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777 6.6 79 770 6 US-11-079-463-8738 Sequence 8738, Ap
1331 6.6 79 771 4 US-10-353-690-110 Sequence 110, App
1331 6.6 79 772 3 US-09-832-292-35 Sequence 35, Appl
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239 6.6 775 775 4 US-10-282-122A-64222 Sequence 64222, A

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977	72.5	6.1	274	4	US-10-425-114-58050	Sequence 58050, A	1050	72	6.0	1035	5	US-10-732-923-1595	Sequence 1595, Ap
978	72.5	6.1	274	4	US-10-425-114-72379	Sequence 72379, A	1051	72	6.0	1275	6	US-11-097-143-3543	Sequence 3543, Ap
979	72.5	6.1	279	4	US-10-424-599-187241	Sequence 187241, A	1052	72	6.0	1275	6	US-09-919-901-2	Sequence 2, Appli
980	72.5	6.1	291	6	US-11-096-568A-22255	Sequence 22255, A	1053	72	6.0	2307	3	US-09-919-901-9	Sequence 9, Appli
981	72.5	6.1	293	4	US-10-424-599-163110	Sequence 163110, A	1054	72	6.0	2307	3	US-09-919-901-16	Sequence 16, Appl
982	72.5	6.1	306	6	US-11-096-568A-22254	Sequence 22254, A	1055	72	6.0	2307	4	US-10-191-966-2	Sequence 2, Appli
983	72.5	6.1	307	4	US-10-425-114-66483	Sequence 66483, A	1056	72	6.0	2307	4	US-10-191-966-9	Sequence 9, Appli
984	72.5	6.1	307	4	US-10-425-114-66808	Sequence 66808, A	1057	72	6.0	2307	4	US-10-191-966-16	Sequence 16, Appl
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986	72.5	6.1	308	4	US-10-425-114-66929	Sequence 66929, A	1059	71.5	6.0	314	5	US-10-291-253A-2496	Sequence 2496, Ap
987	72.5	6.1	310	4	US-10-425-114-66745	Sequence 66745, A	1060	71.5	6.0	348	4	US-10-274-355A-16	Sequence 8, Appli
988	72.5	6.1	310	4	US-10-425-114-67361	Sequence 67361, A	1061	71.5	6.0	363	4	US-10-262-313-8	Sequence 8, Appli
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990	72.5	6.1	312	4	US-10-425-114-66761	Sequence 66761, A	1063	71.5	6.0	366	3	US-09-992-331-8	Sequence 8, Appli
991	72.5	6.1	312	4	US-10-425-114-66930	Sequence 66930, A	1064	71.5	6.0	382	3	US-09-971-228-5	Sequence 5, Appli
992	72.5	6.1	389	4	US-10-225-567A-215	Sequence 215, App	1065	71.5	6.0	382	3	US-09-863-455-2	Sequence 2, Appli
993	72.5	6.1	389	4	US-10-350-924-1	Sequence 1, Appli	1066	71.5	6.0	382	3	US-09-759-514-2	Sequence 2, Appli
994	72.5	6.1	389	5	US-10-756-149-5484	Sequence 5484, Ap	1067	71.5	6.0	382	3	US-09-904-099-1	Sequence 1, Appli

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1069	71.5	6.0	382	4	US-10-225-567A-237	Sequence 237, App	1142	71	5.9	451	5	US-10-732-923-4838	Sequence 4838, App
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1073	71.5	6.0	382	5	US-10-491-545A-30	Sequence 30, Appl	1146	71	5.9	470	4	US-10-176-255-25	Sequence 25, Appl
1074	71.5	6.0	382	5	US-10-498-848-38	Sequence 38, Appl	1147	71	5.9	470	4	US-10-055-555-25	Sequence 25, Appl
1075	71.5	6.0	382	6	US-11-124-368A-173	Sequence 173, App	1148	71	5.9	470	5	US-10-980-560-25	Sequence 25, Appl
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1077	71.5	6.0	382	6	US-11-127-877-58	Sequence 58, Appl	1150	71	5.9	471	3	US-09-929-313-2	Sequence 28, Appl
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1079	71.5	6.0	390	4	US-10-275-984-3	Sequence 3, Appl	1152	71	5.9	471	4	US-10-251-385-122	Sequence 122, App
1080	71.5	6.0	394	4	US-10-394-136-51	Sequence 51, Appl	1153	71	5.9	471	4	US-10-251-385-228	Sequence 228, App
1081	71.5	6.0	405	4	US-10-424-599-149141	Sequence 149141, App	1154	71	5.9	471	4	US-10-225-567A-12	Sequence 12, Appl
1082	71.5	6.0	410	4	US-10-156-761-13608	Sequence 13608, A	1155	71	5.9	471	4	US-10-318-661-22	Sequence 22, Appl
1083	71.5	6.0	433	4	US-10-437-963-156065	Sequence 156065, A	1156	71	5.9	471	4	US-10-092-138-28	Sequence 28, Appl
1084	71.5	6.0	435	6	US-11-045-004-728	Sequence 728, App	1157	71	5.9	471	5	US-10-820-403-28	Sequence 28, Appl
1085	71.5	6.0	448	4	US-10-425-114-55760	Sequence 55760, A	1158	71	5.9	471	5	US-10-741-600-1461	Sequence 1461, App
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1087	71.5	6.0	491	6	US-11-096-568A-29863	Sequence 29863, A	1160	71	5.9	471	5	US-10-741-600-1463	Sequence 1463, App
1088	71.5	6.0	501	6	US-11-188-298-11519	Sequence 11519, A	1161	71	5.9	471	5	US-10-895-789-22	Sequence 22, Appl
1089	71.5	6.0	510	5	US-10-732-923-23578	Sequence 23578, A	1162	71	5.9	471	5	US-10-995-561-901	Sequence 901, App
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1091	71.5	6.0	524	4	US-10-282-122A-53957	Sequence 53957, A	1164	71	5.9	495	4	US-10-437-963-201663	Sequence 201663, A
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1093	71.5	6.0	565	4	US-10-176-847-100	Sequence 100, App	1166	71	5.9	546	4	US-10-369-493-22014	Sequence 22014, A
1094	71.5	6.0	565	6	US-11-080-991-100	Sequence 100, App	1167	71	5.9	559	4	US-10-128-714-8457	Sequence 8457, App
1095	71.5	6.0	568	3	US-09-843-856-2	Sequence 2, Appl	1168	71	5.9	563	4	US-10-139-310-236	Sequence 236, App
1096	71.5	6.0	601	4	US-10-282-122A-44316	Sequence 44316, A	1169	71	5.9	564	5	US-10-968-848-83	Sequence 83, Appl
1097	71.5	6.0	651	6	US-11-096-568A-29862	Sequence 29862, A	1170	71	5.9	629	4	US-10-437-963-119462	Sequence 119462, A
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1101	71.5	6.0	697	6	US-11-119-096-46	Sequence 46, Appl	1174	71	5.9	727	4	US-10-114-270-190	Sequence 190, App
1102	71.5	6.0	698	3	US-09-371-347-2	Sequence 2, Appl	1175	71	5.9	788	4	US-10-335-977-5540	Sequence 5540, App
1103	71.5	6.0	698	3	US-09-371-347-21	Sequence 21, Appl	1176	71	5.9	792	6	US-11-097-143-6948	Sequence 6948, App
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1111	71.5	6.0	698	6	US-11-119-096-42	Sequence 42, Appl	1184	70.5	5.9	147	4	US-10-767-701-60641	Sequence 60641, A
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1114	71.5	6.0	725	5	US-10-995-561-938	Sequence 938, App	1187	70.5	5.9	228	4	US-10-051-902-16	Sequence 16, Appl
1115	71.5	6.0	743	5	US-10-732-923-23563	Sequence 23563, A	1188	70.5	5.9	228	4	US-10-051-909-16	Sequence 16, Appl
1116	71.5	6.0	860	4	US-10-060-425-2	Sequence 2, Appl	1189	70.5	5.9	228	6	US-11-210-316-16	Sequence 16, Appl
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1119	71.5	6.0	2923	3	US-09-916-849A-3	Sequence 3, Appl	1192	70.5	5.9	275	4	US-10-282-122A-45354	Sequence 45354, A
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1124	71.5	6.0	2923	4	US-10-038-854-70	Sequence 70, Appl	1197	70.5	5.9	343	4	US-10-403-142-158	Sequence 158, App
1125	71.5	6.0	2923	6	US-11-200-822-3	Sequence 3, Appl	1198	70.5	5.9	343	5	US-10-453-372-1122	Sequence 1122, App
1126	71.5	6.0	2936	4	US-10-311-623-9	Sequence 9, Appl	1199	70.5	5.9	363	4	US-10-262-313-9	Sequence 9, Appl
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1130	71	5.9	240	4	US-10-262-839-72	Sequence 72, App	1203	70.5	5.9	366	3	US-09-992-331-9	Sequence 9, Appl
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1137	71	5.9	414	5	US-10-732-923-981	Sequence 981, App	1210	70.5	5.9	390	4	US-10-060-902-24	Sequence 24, Appl
1138	71	5.9	423	6	US-11-045-004-1118	Sequence 1118, App	1211	70.5	5.9	390	4	US-10-354-247-22	Sequence 22, Appl
1139	71	5.9	438	4	US-10-437-963-181098	Sequence 181098, App	1212	70.5	5.9	390	4	US-10-354-247-24	Sequence 24, Appl
1140	71	5.9	444	4	US-10-287-226-370	Sequence 370, App	1213	70.5	5.9	393	4	US-10-060-902-28	Sequence 28, Appl

1214	70.5	5.9	393	4	US-10-060-902-36	Sequence 36, Appl	1287	70	5.9	475	6	US-11-096-568A-4755	Sequence 4755, Ap
1215	70.5	5.9	393	4	US-10-354-247-36	Sequence 28, Appl	1288	70	5.9	494	6	US-11-087-099-4883	Sequence 4883, Ap
1216	70.5	5.9	393	4	US-10-354-247-36	Sequence 36, Appl	1289	70	5.9	494	6	US-11-087-099-10612	Sequence 10612, A
1217	70.5	5.9	394	6	US-11-087-099-4992	Sequence 4992, Ap	1290	70	5.9	506	5	US-10-485-517-344	Sequence 344, App
1218	70.5	5.9	402	4	US-10-225-567A-294	Sequence 294, Appl	1291	70	5.9	513	6	US-10-424-599-195511	Sequence 195511
1219	70.5	5.9	402	4	US-10-060-902-34	Sequence 34, Appl	1292	70	5.9	513	6	US-11-087-099-8860	Sequence 8860, Ap
1220	70.5	5.9	402	4	US-10-354-247-34	Sequence 34, Appl	1293	70	5.9	540	5	US-10-343-903-20	Sequence 20, Appl
1221	70.5	5.9	407	4	US-10-060-902-18	Sequence 18, Appl	1294	70	5.9	602	4	US-10-282-122A-46186	Sequence 46186, A
1222	70.5	5.9	407	4	US-10-354-247-18	Sequence 18, Appl	1295	70	5.9	637	4	US-10-282-122A-61377	Sequence 61377, A
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1224	70.5	5.9	425	4	US-10-060-902-26	Sequence 26, Appl	1297	70	5.9	640	6	US-11-123-241-123	Sequence 123, App
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1229	70.5	5.9	494	4	US-10-425-114-65620	Sequence 65620, A	1302	70	5.9	1216	4	US-10-425-115-213298	Sequence 213298
1230	70.5	5.9	496	6	US-11-087-099-948	Sequence 948, App	1303	70	5.9	2738	4	US-10-437-963-118551	Sequence 118551
1231	70.5	5.9	496	6	US-11-188-298-1008	Sequence 1008, Ap	1304	69.5	5.8	138	5	US-10-986-405-286	Sequence 286, App
1232	70.5	5.9	499	4	US-10-724-972A-5387	Sequence 5387, Ap	1305	69.5	5.8	141	4	US-10-115-571A-41	Sequence 41, Appl
1233	70.5	5.9	521	4	US-10-282-122A-58397	Sequence 58397, A	1306	69.5	5.8	141	5	US-10-732-923-4771	Sequence 4771, Ap
1234	70.5	5.9	539	4	US-10-051-902-26	Sequence 26, Appl	1307	69.5	5.8	141	6	US-11-087-099-6202	Sequence 6202, Ap
1235	70.5	5.9	539	4	US-10-051-909-26	Sequence 26, Appl	1308	69.5	5.8	201	5	US-10-501-282-3216	Sequence 3216, Ap
1236	70.5	5.9	539	6	US-11-210-316-26	Sequence 26, Appl	1309	69.5	5.8	206	6	US-11-096-568A-4311	Sequence 4311, Ap
1237	70.5	5.9	548	4	US-10-282-122A-55342	Sequence 55342, A	1310	69.5	5.8	210	3	US-09-811-284-198	Sequence 198, App
1238	70.5	5.9	556	4	US-10-369-493-5442	Sequence 5442, Ap	1311	69.5	5.8	247	5	US-10-501-282-3218	Sequence 3218, Ap
1239	70.5	5.9	599	3	US-09-845-908-11	Sequence 11, Appl	1312	69.5	5.8	253	3	US-09-981-566A-51	Sequence 51, Appl
1240	70.5	5.9	717	3	US-09-925-300-1299	Sequence 1299, Ap	1313	69.5	5.8	257	4	US-10-767-701-45706	Sequence 45706, A
1241	70.5	5.9	740	4	US-10-051-909-37	Sequence 37, Appl	1314	69.5	5.8	261	6	US-11-097-143-14418	Sequence 14418, A
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1244	70.5	5.9	1026	5	US-10-032-585-7591	Sequence 7591, Ap	1317	69.5	5.8	296	4	US-10-746-795-24	Sequence 24, Appl
1245	70.5	5.9	1158	5	US-10-732-923-22552	Sequence 22552, A	1318	69.5	5.8	306	4	US-10-425-115-192496	Sequence 192496
1246	70.5	5.9	1163	4	US-10-336-472-4	Sequence 4, Appli	1319	69.5	5.8	308	3	US-09-886-055-453	Sequence 453, App
1247	70.5	5.9	1781	3	US-09-738-877-3	Sequence 3, Appli	1320	69.5	5.8	308	3	US-09-804-291-453	Sequence 453, App
1248	70.5	5.9	1781	3	US-09-961-403-13	Sequence 13, Appl	1321	69.5	5.8	308	4	US-10-017-161-912	Sequence 912, App
1249	70.5	5.9	1781	4	US-10-428-487-16	Sequence 16, Appl	1322	69.5	5.8	308	4	US-10-044-643-9	Sequence 9, Appl1
1250	70.5	5.9	1781	4	US-10-211-462-44	Sequence 44, Appl	1323	69.5	5.8	308	4	US-10-292-798-786	Sequence 786, App
1251	70.5	5.9	1787	5	US-10-732-923-8682	Sequence 8682, Ap	1324	69.5	5.8	308	4	US-10-343-650A-216	Sequence 216, App
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1256	70.5	5.9	292	4	US-10-251-385-162	Sequence 63601, A	1329	69.5	5.8	330	6	US-11-096-568A-6962	Sequence 6962, Ap
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1422	69	5.8	666	4	US-10-276-774-2139	Sequence 2139, Ap	1495	68.5	5.7	548	4	US-10-440-464-88	Sequence 88, Appl
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SUMMARIES

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26	85.5	7.2	438	US-11-371-354-69179	Sequence 69179, A
27	83.5	7.0	322	US-11-056-3558-23090	Sequence 23090, A
28	81.5	6.8	577	US-11-371-354-67415	Sequence 67415, A

645	6.8	81.5	29	6	US-10-449-902-44461	Sequence 44461, A
473	6.8	81	30	7	US-11-056-3558-86814	Sequence 86814, A
492	6.8	81	31	7	US-11-056-3558-86813	Sequence 86813, A
607	6.8	81	32	7	US-11-056-3558-86812	Sequence 86812, A
322	6.7	80.5	33	7	US-11-056-3558-72028	Sequence 72028, A
536	6.7	80.5	34	7	US-11-450-517-165	Sequence 165, App
238	6.7	80	35	7	US-11-293-697-3158	Sequence 3158, Ap
533	6.7	80	36	6	US-10-953-349-21116	Sequence 21116, A
544	6.7	80	37	6	US-10-953-349-21115	Sequence 21115, A
545	6.7	80	38	6	US-10-953-349-21114	Sequence 21114, A
700	6.7	80	39	7	US-11-357-421-283	Sequence 283, App
596	6.6	78.5	40	7	US-11-371-354-59143	Sequence 59143, A
666	6.6	78.5	41	6	US-10-513-024-36	Sequence 36, Appl
669	6.6	78.5	42	7	US-11-434-137-6624	Sequence 6624, Ap
669	6.6	78.5	43	7	US-11-434-137-8984	Sequence 8984, Ap
669	6.6	78.5	44	7	US-11-434-184-6624	Sequence 6624, Ap
669	6.6	78.5	45	7	US-11-434-184-8984	Sequence 8984, Ap
669	6.6	78.5	46	7	US-11-434-199-6624	Sequence 6624, Ap
669	6.6	78.5	47	7	US-11-434-199-8984	Sequence 8984, Ap
669	6.6	78.5	48	7	US-11-434-203-6624	Sequence 6624, Ap
669	6.6	78.5	49	7	US-11-434-203-8984	Sequence 8984, Ap
669	6.6	78.5	50	7	US-11-434-127-6624	Sequence 6624, Ap
669	6.6	78.5	51	7	US-11-434-127-8984	Sequence 8984, Ap
711	6.6	78.5	52	6	US-10-540-898-70	Sequence 70, Appl
754	6.6	78.5	53	6	US-10-540-898-72	Sequence 72, Appl
376	6.5	77.5	54	6	US-10-449-902-41875	Sequence 41875, A
742	6.5	77.5	55	7	US-11-056-3558-19018	Sequence 19018, A
747	6.5	77.5	56	7	US-11-056-3558-19017	Sequence 19017, A
828	6.5	77.5	57	7	US-11-056-3558-19016	Sequence 19016, A
272	6.4	77	58	7	US-11-305-666-68	Sequence 68, Appl
650	6.4	77	59	6	US-10-471-571A-3906	Sequence 3906, Ap
191	6.4	76.5	61	7	US-11-056-3558-7	Sequence 7, Appli
195	6.4	76.5	62	7	US-11-056-3558-6	Sequence 6, Appli
215	6.4	76.5	63	7	US-11-056-3558-5	Sequence 5, Appli
224	6.4	76.5	64	6	US-10-953-349-15492	Sequence 15492, A
243	6.4	76.5	65	6	US-11-371-354-63461	Sequence 63461, A
364	6.4	76.5	66	6	US-10-612-783-4769	Sequence 4769, Ap
453	6.4	76.5	67	6	US-10-449-902-43999	Sequence 43999, A
526	6.4	76.5	68	6	US-10-533-519-2243	Sequence 2243, Ap
526	6.4	76.5	69	7	US-11-371-354-59907	Sequence 59907, A
570	6.4	76.5	70	7	US-11-371-354-67531	Sequence 67531, A
570	6.4	76.5	71	6	US-11-371-354-77056	Sequence 77056, A
615	6.4	76.5	72	6	US-10-526-324-103	Sequence 103, App
389	6.3	75.5	73	7	US-11-305-666-91	Sequence 91, Appl
342	6.3	75.5	74	7	US-11-158-863-528	Sequence 528, App
356	6.3	75.5	75	7	US-11-366-965-815	Sequence 815, App
215	6.3	75	76	6	US-10-449-902-40201	Sequence 40201, A
288	6.3	75	77	7	US-11-174-307B-5326	Sequence 5326, Ap
288	6.3	75	78	7	US-11-305-666-89	Sequence 89, Appl
289	6.3	75	79	7	US-11-305-666-90	Sequence 90, Appl
476	6.3	75	80	7	US-11-330-403-12095	Sequence 12095, A
278	6.2	74.5	81	6	US-10-449-902-32060	Sequence 32060, A
278	6.2	74.5	82	6	US-10-449-902-49176	Sequence 49176, A
355	6.2	74.5	83	6	US-10-516-032-8	Sequence 8, Appli
355	6.2	74.5	84	6	US-10-533-519-1109	Sequence 1109, Ap
355	6.2	74.5	85	7	US-11-371-354-56785	Sequence 56785, A
793	6.2	74.5	86	7	US-11-330-403-13739	Sequence 13739, A
1084	6.2	74.5	87	6	US-10-449-902-41128	Sequence 41128, A
366	6.2	74	88	6	US-10-471-571A-4838	Sequence 4838, Ap
402	6.2	74	89	6	US-11-056-3558-72132	Sequence 72132, A
458	6.2	74	90	7	US-11-056-3558-72131	Sequence 72131, A
458	6.2	74	91	7	US-11-056-3558-88445	Sequence 88445, A
458	6.2	74	92	7	US-11-056-3558-92201	Sequence 92201, A
487	6.2	74	93	7	US-11-056-3558-72130	Sequence 72130, A
487	6.2	74	94	7	US-11-056-3558-88444	Sequence 88444, A
487	6.2	74	95	7	US-11-056-3558-92200	Sequence 92200, A
497	6.2	74	96	7	US-11-056-3558-88443	Sequence 88443, A
497	6.2	74	97	7	US-11-056-3558-92199	Sequence 92199, A
298	6.2	73.5	98	6	US-10-449-902-47883	Sequence 47883, A
377	6.2	73.5	99	6	US-10-953-349-2568	Sequence 2568, Ap
434	6.2	73.5	100	6	US-10-449-902-51273	Sequence 51273, A
442	6.2	73.5	101	6	US-10-953-349-2567	Sequence 2567, Ap

102	73.5	6.2	489	6	US-10-953-349-2566	Sequence 2566, Ap	175	71	5.9	295	7	US-11-434-199-1686	Sequence 1686, Ap
103	73.5	6.2	491	6	US-10-511-937-2822	Sequence 2522, Ap	176	71	5.9	295	7	US-11-434-203-1686	Sequence 1686, Ap
104	73.5	6.2	491	6	US-10-511-937-2523	Sequence 2523, Ap	177	71	5.9	295	7	US-11-434-127-1686	Sequence 1686, Ap
105	73.5	6.2	491	6	US-10-511-937-2526	Sequence 2526, Ap	178	71	5.9	438	6	US-10-449-902-53385	Sequence 53385, A
106	73.5	6.2	491	6	US-10-511-937-2527	Sequence 2527, Ap	179	71	5.9	483	6	US-11-174-307B-5500	Sequence 5500, Ap
107	73.5	6.2	517	6	US-10-449-902-43559	Sequence 43559, A	180	71	5.9	495	6	US-10-449-902-32757	Sequence 32757, A
108	73.5	6.2	557	7	US-11-056-355B-83002	Sequence 83002, A	181	71	5.9	495	6	US-10-449-902-43122	Sequence 43122, A
109	73.5	6.2	567	7	US-11-056-355B-83001	Sequence 83001, A	182	71	5.9	515	6	US-11-056-355B-69513	Sequence 69513, A
110	73.5	6.2	1095	7	US-11-056-355B-71583	Sequence 71583, A	183	71	5.9	543	6	US-10-449-902-52957	Sequence 52957, A
111	73.5	6.2	1107	7	US-11-056-355B-73209	Sequence 73209, A	184	71	5.9	543	6	US-10-449-902-52964	Sequence 52964, A
112	73.5	6.2	1207	6	US-10-449-902-53308	Sequence 53308, A	185	71	5.9	646	7	US-11-056-355B-69512	Sequence 69512, A
113	73.5	6.2	7176	6	US-10-822-303-9897	Sequence 9897, Ap	186	71	5.9	676	7	US-11-056-355B-69511	Sequence 69511, A
114	73	6.1	249	7	US-11-434-184-7910	Sequence 7910, Ap	187	71	5.9	825	7	US-11-056-355B-69916	Sequence 69916, A
115	73	6.1	249	7	US-11-434-184-7910	Sequence 7910, Ap	188	71	5.9	826	7	US-11-056-355B-69915	Sequence 69915, A
116	73	6.1	249	7	US-11-434-199-7910	Sequence 7910, Ap	189	71	5.9	830	6	US-11-056-355B-69914	Sequence 69914, A
117	73	6.1	249	7	US-11-434-203-7910	Sequence 7910, Ap	190	71	5.9	848	6	US-10-449-902-45336	Sequence 45336, A
118	73	6.1	249	6	US-11-434-127-7910	Sequence 7910, Ap	191	70.5	5.9	374	7	US-11-371-354-59287	Sequence 59287, A
119	73	6.1	290	6	US-10-471-571A-4788	Sequence 4788, Ap	192	70.5	5.9	402	6	US-10-530-187-264	Sequence 264, App
120	73	6.1	415	7	US-11-056-355B-82151	Sequence 82151, A	193	70.5	5.9	620	7	US-11-056-355B-88722	Sequence 88722, A
121	73	6.1	472	7	US-11-056-355B-82150	Sequence 82150, A	194	70.5	5.9	620	7	US-11-056-355B-92478	Sequence 92478, A
122	73	6.1	474	7	US-11-056-355B-82149	Sequence 82149, A	195	70.5	5.9	622	7	US-11-056-355B-88721	Sequence 88721, A
123	73	6.1	474	7	US-11-330-403-16009	Sequence 16009, A	196	70.5	5.9	622	7	US-11-056-355B-92477	Sequence 92477, A
124	73	6.1	494	6	US-10-449-902-54489	Sequence 54489, A	197	70.5	5.9	623	7	US-11-056-355B-70840	Sequence 70840, A
125	73	6.1	494	6	US-11-251-465-17	Sequence 17, Appl	198	70.5	5.9	697	7	US-11-056-355B-70839	Sequence 70839, A
126	73	6.1	792	6	US-10-471-571A-4714	Sequence 4714, Ap	199	70.5	5.9	697	7	US-11-056-355B-88720	Sequence 88720, A
127	73	6.1	1314	6	US-10-449-902-41194	Sequence 41194, A	200	70.5	5.9	697	7	US-11-056-355B-92476	Sequence 92476, A
128	72.5	6.1	209	6	US-10-953-349-2299	Sequence 2299, Ap	201	70.5	5.9	700	7	US-11-056-355B-70838	Sequence 70838, A
129	72.5	6.1	209	7	US-11-056-355B-40232	Sequence 40232, A	202	70	5.9	185	7	US-11-056-355B-26745	Sequence 26745, A
130	72.5	6.1	209	7	US-11-056-355B-103777	Sequence 103777, A	203	70	5.9	185	7	US-11-056-355B-30003	Sequence 30003, A
131	72.5	6.1	209	7	US-11-056-355B-115016	Sequence 115016, A	204	70	5.9	189	7	US-11-056-355B-33593	Sequence 33593, A
132	72.5	6.1	216	7	US-11-056-355B-103776	Sequence 103776, A	205	70	5.9	189	7	US-11-056-355B-26744	Sequence 26744, A
133	72.5	6.1	216	7	US-11-056-355B-115015	Sequence 115015, A	206	70	5.9	189	7	US-11-056-355B-30002	Sequence 30002, A
134	72.5	6.1	278	7	US-11-330-403-9646	Sequence 9646, Ap	207	70	5.9	189	7	US-11-056-355B-33592	Sequence 33592, A
135	72.5	6.1	291	7	US-11-056-355B-7634	Sequence 7634, Ap	208	70	5.9	235	7	US-11-056-355B-26743	Sequence 26743, A
136	72.5	6.1	291	7	US-11-305-666-67	Sequence 67, Appl	209	70	5.9	235	7	US-11-056-355B-30001	Sequence 30001, A
137	72.5	6.1	291	7	US-11-305-666-86	Sequence 86, Appl	210	70	5.9	235	7	US-11-056-355B-33591	Sequence 33591, A
138	72.5	6.1	291	7	US-11-305-666-87	Sequence 87, Appl	211	70	5.9	274	7	US-11-056-355B-34997	Sequence 34997, A
139	72.5	6.1	291	7	US-11-305-666-88	Sequence 88, Appl	212	70	5.9	274	7	US-11-056-355B-76301	Sequence 76301, A
140	72.5	6.1	306	6	US-11-056-355B-7633	Sequence 7633, Ap	213	70	5.9	274	7	US-11-056-355B-77453	Sequence 77453, A
141	72.5	6.1	389	6	US-10-565-487-1	Sequence 1, Appl	214	70	5.9	274	7	US-11-056-355B-104540	Sequence 104540, A
142	72.5	6.1	389	6	US-10-565-487-8	Sequence 8, Appl	215	70	5.9	287	7	US-11-056-355B-115779	Sequence 115779, A
143	72.5	6.1	389	6	US-10-449-902-55531	Sequence 55531, A	216	70	5.9	287	7	US-11-056-355B-34996	Sequence 34996, A
144	72	6.0	378	6	US-10-669-920-493	Sequence 493, App	217	70	5.9	287	7	US-11-056-355B-76300	Sequence 76300, A
145	72	6.0	378	6	US-10-669-920-495	Sequence 495, App	218	70	5.9	287	7	US-11-056-355B-77452	Sequence 77452, A
146	72	6.0	398	7	US-11-056-355B-90585	Sequence 90585, A	219	70	5.9	287	7	US-11-056-355B-104539	Sequence 104539, A
147	72	6.0	398	7	US-11-056-355B-94341	Sequence 94341, A	220	70	5.9	287	7	US-11-056-355B-115778	Sequence 115778, A
148	72	6.0	447	6	US-10-471-571A-4130	Sequence 4130, Ap	221	70	5.9	367	7	US-11-056-355B-32778	Sequence 32778, Ap
149	72	6.0	461	7	US-11-056-355B-90584	Sequence 90584, A	222	70	5.9	393	7	US-11-056-355B-32777	Sequence 32777, Ap
150	72	6.0	461	7	US-11-056-355B-94340	Sequence 94340, A	223	70	5.9	393	7	US-11-371-354-74527	Sequence 74527, A
151	72	6.0	468	7	US-11-056-355B-94339	Sequence 94339, A	224	70	5.9	475	6	US-10-953-349-17159	Sequence 17159, A
152	72	6.0	495	6	US-10-953-349-6931	Sequence 6931, Ap	225	70	5.9	506	6	US-10-471-571A-3308	Sequence 3308, Ap
153	72	6.0	497	6	US-10-953-349-6930	Sequence 6930, Ap	226	70	5.9	532	7	US-11-330-403-16523	Sequence 16523, A
154	72	6.0	507	6	US-10-953-349-6929	Sequence 6929, Ap	227	70	5.9	1049	6	US-10-556-060-376	Sequence 276, App
155	72	6.0	523	7	US-11-371-354-65085	Sequence 65085, A	228	70	5.9	1049	6	US-10-556-060-451	Sequence 451, App
156	72	6.0	742	6	US-10-518-941-26	Sequence 26, Appl	229	70	5.9	1049	6	US-10-556-060-457	Sequence 457, App
157	72	6.0	746	6	US-10-612-783-4287	Sequence 4287, Ap	230	70	5.9	206	6	US-10-953-349-15493	Sequence 15493, A
158	72	6.0	198	7	US-11-371-354-64751	Sequence 64751, A	231	69.5	5.8	296	7	US-11-357-566-24	Sequence 24, Appl
159	71.5	6.0	218	7	US-11-056-355B-23091	Sequence 23091, A	232	69.5	5.8	317	7	US-11-056-355B-91422	Sequence 91422, A
160	71.5	6.0	282	7	US-11-371-354-60249	Sequence 60249, A	233	69.5	5.8	317	7	US-11-056-355B-95178	Sequence 95178, A
161	71.5	6.0	472	7	US-11-056-355B-72423	Sequence 72423, A	234	69.5	5.8	354	6	US-10-516-032-12	Sequence 12, Appl
162	71.5	6.0	491	7	US-11-056-355B-72422	Sequence 72422, A	235	69.5	5.8	371	7	US-11-056-355B-9101	Sequence 9101, Ap
163	71.5	6.0	510	7	US-11-330-403-17869	Sequence 17869, A	236	69.5	5.8	381	7	US-11-056-355B-9100	Sequence 9100, Ap
164	71.5	6.0	603	6	US-10-471-571A-3718	Sequence 3718, Ap	237	69.5	5.8	430	7	US-11-056-355B-9099	Sequence 9099, Ap
165	71.5	6.0	651	7	US-11-056-355B-72421	Sequence 72421, A	238	69.5	5.8	453	7	US-11-330-403-8969	Sequence 8969, Ap
166	71.5	6.0	890	6	US-10-570-909-67	Sequence 67, Appl	239	69.5	5.8	476	7	US-11-056-355B-91576	Sequence 91576, A
167	71.5	6.0	890	7	US-11-371-354-63449	Sequence 63449, A	240	69.5	5.8	476	7	US-11-056-355B-95332	Sequence 95332, A
168	71.5	6.0	923	6	US-10-570-909-35	Sequence 35, Appl	241	69.5	5.8	503	7	US-11-056-355B-95331	Sequence 95331, A
169	71.5	6.0	2923	6	US-10-570-909-39	Sequence 39, Appl	242	69.5	5.8	503	7	US-11-056-355B-95330	Sequence 95330, A
170	71.5	6.0	276	7	US-11-056-355B-44017	Sequence 44017, A	243	69.5	5.8	534	7	US-11-056-355B-91574	Sequence 91574, A
171	71	5.9	290	7	US-11-056-355B-44016	Sequence 44016, A	244	69.5	5.8	534	7	US-11-056-355B-95330	Sequence 95330, A
172	71	5.9	295	7	US-11-434-137-1686	Sequence 1686, Ap	245	69.5	5.8	557	6	US-10-533-519-995	Sequence 995, App
173	71	5.9	295	7	US-11-434-184-1686	Sequence 1686, Ap	246	69.5	5.8	557	6	US-10-533-519-995	Sequence 995, App
174	71	5.9	295	7	US-11-434-184-1686	Sequence 1686, Ap	247	69.5	5.8	557	7	US-11-318-813-4	Sequence 4, Appl

248	69.5	5.8	557	7	US-11-371-354-57971	Sequence 57971, A	321	68.5	5.7	894	7	US-11-434-127-8898	Sequence 8898, Ap
249	69.5	5.8	584	7	US-11-330-403-17971	Sequence 17971, A	322	68	5.7	247	6	US-10-805-394-5109	Sequence 5109, Ap
250	69.5	5.8	599	7	US-11-302-678-5	Sequence 5, Appli	323	68	5.7	282	6	US-10-513-024-764	Sequence 764, App
251	69.5	5.8	1704	6	US-10-570-909-103	Sequence 103, App	324	68	5.7	295	7	US-11-293-697-4304	Sequence 4304, Ap
252	69.5	5.8	1704	6	US-11-289-102-341	Sequence 341, App	325	68	5.7	312	6	US-10-449-902-43616	Sequence 43616, A
253	69	5.8	200	7	US-11-056-355B-71812	Sequence 71812, A	326	68	5.7	330	6	US-10-953-349-5614	Sequence 5614, Ap
254	69	5.8	214	7	US-11-293-697-2534	Sequence 2534, App	327	68	5.7	330	7	US-11-056-355B-23626	Sequence 23626, A
255	69	5.8	239	6	US-10-526-324-736	Sequence 736, App	328	68	5.7	330	7	US-11-056-355B-36303	Sequence 36303, A
256	69	5.8	252	7	US-11-056-355B-71811	Sequence 71811, A	329	68	5.7	330	7	US-11-403-051-2	Sequence 2, Appli
257	69	5.8	290	7	US-11-305-666-65	Sequence 65, Appli	330	68	5.7	341	7	US-11-403-051-55	Sequence 55, Appli
258	69	5.8	290	7	US-11-305-666-83	Sequence 83, Appli	331	68	5.7	342	6	US-10-449-902-43901	Sequence 43901, A
259	69	5.8	326	7	US-11-056-355B-71810	Sequence 71810, A	332	68	5.7	344	7	US-11-434-137-396	Sequence 396, App
260	69	5.8	350	6	US-10-471-571A-4042	Sequence 4042, Ap	333	68	5.7	344	7	US-11-434-184-396	Sequence 396, App
261	69	5.8	355	6	US-10-449-902-50010	Sequence 50010, A	334	68	5.7	344	7	US-11-434-199-396	Sequence 396, App
262	69	5.8	370	7	US-11-371-354-68363	Sequence 68363, A	335	68	5.7	344	7	US-11-434-203-396	Sequence 396, App
263	69	5.8	440	6	US-10-953-349-22057	Sequence 22057, A	336	68	5.7	344	7	US-11-434-127-396	Sequence 396, App
264	69	5.8	440	6	US-11-056-355B-58390	Sequence 58390, A	337	68	5.7	346	7	US-11-403-051-30	Sequence 30, Appli
265	69	5.8	450	6	US-10-953-349-22056	Sequence 22056, A	338	68	5.7	346	7	US-11-371-354-68411	Sequence 68411, A
266	69	5.8	450	7	US-11-056-355B-58389	Sequence 58389, A	339	68	5.7	355	7	US-11-363-149-84	Sequence 84, Appli
267	69	5.8	453	6	US-10-953-349-5613	Sequence 5613, Ap	340	68	5.7	355	7	US-11-363-151-84	Sequence 84, Appli
268	69	5.8	508	7	US-11-056-355B-36302	Sequence 36302, A	341	68	5.7	355	7	US-11-371-354-68509	Sequence 68509, A
269	69	5.8	520	6	US-10-953-349-5612	Sequence 5612, Ap	342	68	5.7	388	6	US-10-449-902-49827	Sequence 49827, A
270	69	5.8	520	7	US-11-056-355B-36301	Sequence 36301, A	343	68	5.7	389	6	US-10-526-324-1437	Sequence 1437, Ap
271	69	5.8	520	7	US-11-330-403-8817	Sequence 8817, Ap	344	68	5.7	488	7	US-11-242-505A-30	Sequence 30, Appli
272	69	5.8	526	7	US-11-024-544A-12	Sequence 12, Appli	345	68	5.7	488	7	US-11-404-939-561	Sequence 561, App
273	69	5.8	526	7	US-11-024-544A-14	Sequence 14, Appli	346	68	5.7	689	6	US-10-449-902-45629	Sequence 45629, A
274	69	5.8	526	7	US-11-190-750-80	Sequence 80, Appli	347	68	5.7	689	6	US-10-449-902-47834	Sequence 47834, A
275	69	5.8	526	7	US-11-190-750-84	Sequence 84, Appli	348	68	5.7	694	7	US-11-056-355B-72708	Sequence 72708, A
276	69	5.8	526	7	US-11-264-784-82	Sequence 82, Appli	349	68	5.7	710	7	US-11-056-355B-72707	Sequence 72707, A
277	69	5.8	526	7	US-11-264-737-123	Sequence 123, App	350	68	5.7	717	7	US-11-371-354-58891	Sequence 58891, A
278	69	5.8	526	7	US-11-265-761-95	Sequence 95, Appli	351	68	5.7	717	7	US-11-371-354-76500	Sequence 76500, A
279	69	5.8	526	6	US-10-449-902-36835	Sequence 36835, A	352	68	5.7	734	7	US-11-371-354-60363	Sequence 60363, A
280	69	5.8	569	6	US-10-449-902-48588	Sequence 48588, A	353	68	5.7	804	7	US-11-056-355B-72706	Sequence 72706, A
281	69	5.8	569	6	US-10-449-902-50306	Sequence 50306, A	354	68	5.7	1375	6	US-10-449-902-50506	Sequence 50506, A
282	69	5.8	569	6	US-10-449-902-50472	Sequence 50472, A	355	68	5.7	2359	6	US-10-543-503-134	Sequence 134, App
283	69	5.8	647	7	US-11-330-403-5831	Sequence 5831, Ap	356	68	5.7	3010	7	US-11-140-487A-770	Sequence 770, App
284	68.5	5.7	211	7	US-11-199-489A-94	Sequence 94, Appli	357	68	5.7	3010	7	US-11-140-487A-770	Sequence 770, App
285	68.5	5.7	218	7	US-11-056-355B-72029	Sequence 72029, A	358	67.5	5.6	175	7	US-11-371-354-61945	Sequence 61945, A
286	68.5	5.7	220	7	US-11-056-355B-91424	Sequence 91424, A	359	67.5	5.6	213	7	US-11-056-355B-23092	Sequence 23092, A
287	68.5	5.7	220	7	US-11-056-355B-95180	Sequence 95180, A	360	67.5	5.6	250	6	US-10-449-902-49321	Sequence 49321, A
288	68.5	5.7	227	7	US-11-333-747A-144	Sequence 144, App	361	67.5	5.6	286	7	US-11-056-355B-51767	Sequence 51767, A
289	68.5	5.7	228	7	US-11-305-666-77	Sequence 77, Appli	362	67.5	5.6	286	7	US-11-305-666-64	Sequence 64, Appli
290	68.5	5.7	233	7	US-11-056-355B-91423	Sequence 91423, A	363	67.5	5.6	286	7	US-11-305-666-82	Sequence 82, Appli
291	68.5	5.7	233	7	US-11-056-355B-95179	Sequence 95179, A	364	67.5	5.6	292	7	US-11-056-355B-11207	Sequence 11207, A
292	68.5	5.7	287	7	US-11-305-666-85	Sequence 85, Appli	365	67.5	5.6	321	7	US-11-056-355B-11206	Sequence 11206, A
293	68.5	5.7	378	6	US-10-669-920-490	Sequence 490, App	366	67.5	5.6	337	6	US-10-526-324-1564	Sequence 1564, Ap
294	68.5	5.7	435	7	US-11-056-355B-91465	Sequence 91465, A	367	67.5	5.6	348	6	US-10-449-902-43070	Sequence 43070, A
295	68.5	5.7	435	7	US-11-056-355B-95221	Sequence 95221, A	368	67.5	5.6	350	7	US-11-268-745-38	Sequence 38, Appli
296	68.5	5.7	444	7	US-11-358-841-2	Sequence 2, Appli	369	67.5	5.6	354	7	US-11-056-355B-11205	Sequence 11205, A
297	68.5	5.7	468	7	US-11-404-939-553	Sequence 553, App	370	67.5	5.6	387	7	US-11-107-336-44	Sequence 44, Appli
298	68.5	5.7	500	7	US-11-056-355B-91464	Sequence 91464, A	371	67.5	5.6	431	7	US-11-434-137-3244	Sequence 3244, Ap
299	68.5	5.7	500	7	US-11-056-355B-95220	Sequence 95220, A	372	67.5	5.6	431	7	US-11-434-184-3244	Sequence 3244, Ap
300	68.5	5.7	501	6	US-10-449-902-46991	Sequence 46991, A	373	67.5	5.6	431	7	US-11-434-199-3244	Sequence 3244, Ap
301	68.5	5.7	501	7	US-11-056-355B-91477	Sequence 91477, A	374	67.5	5.6	431	7	US-11-434-203-3244	Sequence 3244, Ap
302	68.5	5.7	501	7	US-11-056-355B-95233	Sequence 95233, A	375	67.5	5.6	431	7	US-11-434-127-3244	Sequence 3244, Ap
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304	68.5	5.7	528	7	US-11-056-355B-79431	Sequence 79431, A	377	67.5	5.6	534	7	US-11-434-184-2878	Sequence 2878, Ap
305	68.5	5.7	548	7	US-11-371-354-69559	Sequence 69559, A	378	67.5	5.6	534	7	US-11-434-199-2878	Sequence 2878, Ap
306	68.5	5.7	590	7	US-11-056-355B-79430	Sequence 79430, A	379	67.5	5.6	534	7	US-11-434-203-2878	Sequence 2878, Ap
307	68.5	5.7	643	7	US-11-056-355B-91476	Sequence 91476, A	380	67.5	5.6	534	7	US-11-434-127-2878	Sequence 2878, Ap
308	68.5	5.7	643	7	US-11-056-355B-95232	Sequence 95232, A	381	67.5	5.6	608	7	US-11-293-697-4385	Sequence 4385, Ap
309	68.5	5.7	653	7	US-11-056-355B-91475	Sequence 91475, A	382	67.5	5.6	805	7	US-11-371-354-56443	Sequence 56443, A
310	68.5	5.7	653	7	US-11-056-355B-95231	Sequence 95231, A	383	67.5	5.6	933	7	US-11-226-554-138	Sequence 138, App
311	68.5	5.7	837	7	US-11-371-354-61825	Sequence 61825, A	384	67.5	5.6	933	7	US-11-248-718-138	Sequence 138, App
312	68.5	5.7	894	7	US-11-434-137-5482	Sequence 5482, Ap	385	67.5	5.6	2158	6	US-10-502-394-34	Sequence 34, Appli
313	68.5	5.7	894	7	US-11-434-137-8898	Sequence 8898, Ap	386	67.5	5.6	2265	6	US-10-502-394-35	Sequence 35, Appli
314	68.5	5.7	894	7	US-11-434-184-5482	Sequence 5482, Ap	387	67.5	5.6	2365	6	US-10-533-519-1855	Sequence 1855, Ap
315	68.5	5.7	894	7	US-11-434-184-8898	Sequence 8898, Ap	388	67.5	5.6	2697	6	US-10-502-394-12	Sequence 12, Appli
316	68.5	5.7	894	7	US-11-434-199-5482	Sequence 5482, Ap	389	67.5	5.6	3302	6	US-10-526-109-1	Sequence 1, Appli
317	68.5	5.7	894	7	US-11-434-199-8898	Sequence 8898, Ap	390	67	5.6	158	7	US-11-434-137-2484	Sequence 2484, Ap
318	68.5	5.7	894	7	US-11-434-203-5482	Sequence 5482, Ap	391	67	5.6	158	7	US-11-434-184-2484	Sequence 2484, Ap
319	68.5	5.7	894	7	US-11-434-203-8898	Sequence 8898, Ap	392	67	5.6	158	7	US-11-434-199-2484	Sequence 2484, Ap
320	68.5	5.7	894	7	US-11-434-127-5482	Sequence 5482, Ap	393	67	5.6	158	7	US-11-434-203-2484	Sequence 2484, Ap

394	67	5.6	158	7	US-11-434-127-2484	Sequence 2484, Ap	467	66	5.5	151	7	US-11-366-965-1129	Sequence 1129, Ap
395	67	5.6	166	7	US-11-174-307B-5012	Sequence 5012, Ap	468	66	5.5	217	6	US-10-953-349-28671	Sequence 28671, A
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398	67	5.6	179	7	US-11-056-355B-103778	Sequence 103778, A	471	66	5.5	238	7	US-11-056-355B-105779	Sequence 105779, A
399	67	5.6	179	7	US-11-056-355B-115017	Sequence 115017, A	472	66	5.5	238	7	US-11-056-355B-17018	Sequence 17018, A
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403	67	5.6	287	7	US-11-434-199-3540	Sequence 3540, Ap	476	66	5.5	377	7	US-11-357-204-9	Sequence 9, Appl
404	67	5.6	287	7	US-11-434-127-3540	Sequence 3540, Ap	477	66	5.5	389	7	US-11-434-137-5792	Sequence 5792, Ap
405	67	5.6	290	6	US-10-449-902-31146	Sequence 31146, A	478	66	5.5	389	7	US-11-434-184-5792	Sequence 5792, Ap
406	67	5.6	295	7	US-11-056-355B-8466	Sequence 8466, Ap	479	66	5.5	389	7	US-11-434-199-5792	Sequence 5792, Ap
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408	67	5.6	320	7	US-11-434-184-3596	Sequence 3596, Ap	481	66	5.5	389	7	US-11-434-127-5792	Sequence 5792, Ap
409	67	5.6	320	7	US-11-434-199-3596	Sequence 3596, Ap	482	66	5.5	405	7	US-11-412-025-38	Sequence 38, Appl
410	67	5.6	320	7	US-11-434-203-3596	Sequence 3596, Ap	483	66	5.5	410	7	US-11-366-965-908	Sequence 908, App
411	67	5.6	320	7	US-11-434-127-3596	Sequence 3596, Ap	484	66	5.5	412	6	US-10-471-571A-2744	Sequence 2744, Ap
412	67	5.6	457	7	US-11-056-355B-50170	Sequence 50170, A	485	66	5.5	447	6	US-10-538-198-2	Sequence 2, Appl
413	67	5.6	457	7	US-11-056-355B-78769	Sequence 78769, A	486	66	5.5	450	6	US-10-538-198-4	Sequence 4, Appl
414	67	5.6	465	7	US-11-056-355B-50169	Sequence 50169, A	487	66	5.5	461	6	US-10-805-394-5041	Sequence 5041, Ap
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418	67	5.6	496	7	US-11-371-354-64037	Sequence 64037, A	491	66	5.5	3499	7	US-11-063-439-222	Sequence 222, App
419	67	5.6	498	6	US-10-449-902-5253	Sequence 5253, A	492	66	5.5	3507	7	US-11-063-439-215	Sequence 215, App
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422	67	5.6	746	7	US-11-056-355B-87569	Sequence 87569, A	495	65.5	5.5	304	6	US-10-805-394-6200	Sequence 6200, Ap
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431	67	5.6	1851	7	US-11-056-355B-75727	Sequence 75727, A	504	65.5	5.5	718	6	US-10-533-519-1798	Sequence 1798, Ap
432	67	5.6	1856	7	US-11-056-355B-87719	Sequence 87719, A	505	65.5	5.5	740	7	US-11-251-208-230	Sequence 230, App
433	67	5.6	3010	7	US-11-119-587A-8	Sequence 8, Appl	506	65.5	5.5	801	6	US-10-471-571A-258	Sequence 258, App
434	67	5.6	3502	7	US-11-063-439-160	Sequence 160, App	507	65.5	5.5	838	7	US-11-346-489-5	Sequence 5, Appl
435	66.5	5.6	198	7	US-11-056-355B-28244	Sequence 28244, A	508	65.5	5.5	860	6	US-10-530-187-282	Sequence 282, App
436	66.5	5.6	198	7	US-11-056-355B-31834	Sequence 31834, A	509	65.5	5.5	935	7	US-11-371-354-55369	Sequence 55369, A
437	66.5	5.6	198	7	US-11-056-355B-77217	Sequence 77217, A	510	65.5	5.5	935	7	US-11-226-554-148	Sequence 148, App
438	66.5	5.6	304	7	US-11-371-354-66893	Sequence 66893, A	511	65.5	5.5	1143	7	US-11-248-718-148	Sequence 148, App
439	66.5	5.6	359	6	US-10-471-571A-3590	Sequence 3590, Ap	512	65.5	5.5	1146	7	US-11-274-081-3	Sequence 3, Appl
440	66.5	5.6	371	6	US-10-953-349-34722	Sequence 34722, A	513	65.5	5.5	1152	7	US-11-226-554-147	Sequence 147, App
441	66.5	5.6	384	6	US-10-505-928-263	Sequence 263, App	514	65.5	5.5	1152	7	US-11-248-718-147	Sequence 147, App
442	66.5	5.6	384	6	US-10-511-937-2532	Sequence 2532, Ap	515	65.5	5.5	1427	6	US-10-309-407-354	Sequence 354, App
443	66.5	5.6	384	6	US-10-953-349-34721	Sequence 34721, A	516	65	5.4	176	7	US-11-301-309-22	Sequence 22, Appl
444	66.5	5.6	392	7	US-11-330-403-11138	Sequence 11138, A	517	65	5.4	179	7	US-11-434-137-6692	Sequence 6692, Ap
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447	66.5	5.6	453	6	US-10-449-902-52191	Sequence 52191, A	520	65	5.4	179	7	US-11-434-203-6692	Sequence 6692, Ap
448	66.5	5.6	453	7	US-11-330-403-3789	Sequence 3789, Ap	521	65	5.4	179	7	US-11-434-127-6692	Sequence 6692, Ap
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451	66.5	5.6	459	6	US-10-612-783-4310	Sequence 4310, Ap	524	65	5.4	202	7	US-11-434-184-9336	Sequence 9336, Ap
452	66.5	5.6	499	7	US-11-434-137-3562	Sequence 3562, Ap	525	65	5.4	202	7	US-11-434-199-9336	Sequence 9336, Ap
453	66.5	5.6	499	7	US-11-434-184-3562	Sequence 3562, Ap	526	65	5.4	202	7	US-11-434-203-9336	Sequence 9336, Ap
454	66.5	5.6	499	7	US-11-434-199-3562	Sequence 3562, Ap	527	65	5.4	202	7	US-11-434-127-9336	Sequence 9336, Ap
455	66.5	5.6	499	7	US-11-434-203-3562	Sequence 3562, Ap	528	65	5.4	225	6	US-10-822-303-6074	Sequence 6074, Ap
456	66.5	5.6	499	7	US-11-434-127-3562	Sequence 3562, Ap	529	65	5.4	271	6	US-10-471-571A-5458	Sequence 5458, Ap
457	66.5	5.6	504	6	US-10-449-902-36972	Sequence 36972, A	530	65	5.4	277	6	US-10-533-519-333	Sequence 333, App
458	66.5	5.6	550	6	US-10-533-519-2434	Sequence 2434, Ap	531	65	5.4	290	6	US-10-449-902-28559	Sequence 28559, A
459	66.5	5.6	551	6	US-10-570-909-4	Sequence 4, Appl	532	65	5.4	290	6	US-10-449-902-28581	Sequence 28581, A
460	66.5	5.6	772	6	US-10-540-898-67	Sequence 67, Appl	533	65	5.4	290	6	Sequence 32480, A	Sequence 32480, A
461	66.5	5.6	830	6	US-10-511-937-2474	Sequence 2474, Ap	534	65	5.4	290	6	Sequence 45137, A	Sequence 45137, A
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463	66.5	5.6	1383	7	US-11-301-094-2	Sequence 2, Appl	536	65	5.4	305	7	Sequence 1067, Ap	Sequence 1067, Ap
464	66.5	5.6	1530	6	US-10-449-902-41309	Sequence 41309, A	537	65	5.4	325	6	Sequence 6641, Ap	Sequence 6641, Ap
465	66.5	5.6	3010	6	US-10-534-774-24	Sequence 24, Appl	538	65	5.4	325	7	Sequence 23421, A	Sequence 23421, A
466	66.5	5.6	3010	6	US-10-535-047-24	Sequence 24, Appl	539	65	5.4	325	7	Sequence 25643, A	Sequence 25643, A

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542	65	5.4	375	7	US-11-358-841-3	Sequence 3, Appli	615	64.5	5.4	413	7	US-11-412-025-32	Sequence 32, Appl
543	65	5.4	375	7	US-11-412-025-6	Sequence 6, Appli	616	64.5	5.4	425	7	US-11-056-355B-106592	Sequence 106592,
544	65	5.4	401	7	US-11-358-841-4	Sequence 4, Appli	617	64.5	5.4	425	7	US-11-056-355B-117831	Sequence 117831,
545	65	5.4	401	7	US-11-412-025-8	Sequence 8, Appli	618	64.5	5.4	437	7	US-11-056-355B-81935	Sequence 81935, A
546	65	5.4	403	7	US-11-371-354-58649	Sequence 58649, A	619	64.5	5.4	479	7	US-11-371-354-63789	Sequence 63789, A
547	65	5.4	415	7	US-11-358-841-1	Sequence 1, Appli	620	64.5	5.4	495	6	US-10-953-349-13164	Sequence 13164, A
548	65	5.4	415	7	US-11-404-939-483	Sequence 483, App	621	64.5	5.4	507	7	US-11-330-403-13164	Sequence 13164, A
549	65	5.4	415	7	US-11-412-025-2	Sequence 2, Appli	622	64.5	5.4	507	7	US-11-330-403-13163	Sequence 13163, A
550	65	5.4	415	7	US-11-412-025-4	Sequence 4, Appli	623	64.5	5.4	513	6	US-10-953-349-10101	Sequence 10101, A
551	65	5.4	415	7	US-11-412-025-40	Sequence 40, Appl	624	64.5	5.4	529	7	US-11-056-355B-50367	Sequence 50367, A
552	65	5.4	415	7	US-11-371-354-69987	Sequence 69987, A	625	64.5	5.4	529	7	US-11-056-355B-86281	Sequence 86281, A
553	65	5.4	444	6	US-10-533-519-10077	Sequence 10077, Ap	626	64.5	5.4	538	6	US-10-953-349-10100	Sequence 10100, A
554	65	5.4	477	7	US-11-330-403-2009	Sequence 2009, Ap	627	64.5	5.4	538	7	US-11-056-355B-50366	Sequence 50366, A
555	65	5.4	490	7	US-11-330-403-1544	Sequence 1544, Ap	628	64.5	5.4	538	7	US-11-056-355B-86280	Sequence 86280, A
556	65	5.4	523	6	US-10-449-902-35714	Sequence 35714, Ap	629	64.5	5.4	567	7	US-11-444-093-12	Sequence 12, Appl
557	65	5.4	530	6	US-10-471-571A-4590	Sequence 4590, Ap	630	64.5	5.4	567	7	US-11-474-663-7	Sequence 7, Appli
558	65	5.4	547	7	US-11-158-863-186	Sequence 186, App	631	64.5	5.4	593	6	US-10-953-349-10099	Sequence 10099, A
559	65	5.4	560	7	US-11-317-847A-144	Sequence 144, App	632	64.5	5.4	593	7	US-11-056-355B-50365	Sequence 50365, A
560	65	5.4	614	7	US-11-317-847A-146	Sequence 146, App	633	64.5	5.4	593	7	US-11-056-355B-86279	Sequence 86279, A
561	65	5.4	625	7	US-11-330-403-1652	Sequence 1652, Ap	634	64.5	5.4	614	6	US-10-471-571A-4852	Sequence 4852, Ap
562	65	5.4	661	7	US-11-056-355B-107830	Sequence 107830,	635	64.5	5.4	632	6	US-10-953-349-12946	Sequence 12946, A
563	65	5.4	661	7	US-11-056-355B-119069	Sequence 119069,	636	64.5	5.4	635	6	US-10-953-349-12945	Sequence 12945, A
564	65	5.4	673	7	US-11-056-355B-107829	Sequence 107829,	637	64.5	5.4	644	6	US-10-953-349-12944	Sequence 12944, A
565	65	5.4	673	7	US-11-056-355B-119068	Sequence 119068,	638	64.5	5.4	803	6	US-10-553-928-215	Sequence 215, App
566	65	5.4	677	7	US-11-056-355B-90067	Sequence 90067, A	639	64.5	5.4	1865	7	US-11-247-437-8	Sequence 8, Appli
567	65	5.4	677	7	US-11-056-355B-93823	Sequence 93823, A	640	64.5	5.4	3195	7	US-11-330-403-18988	Sequence 18988, A
568	65	5.4	686	7	US-11-056-355B-90066	Sequence 90066, A	641	64.5	5.4	3195	7	US-11-330-403-18988	Sequence 18988, A
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570	65	5.4	801	6	US-10-953-349-5006	Sequence 5006, Ap	643	64.5	5.4	206	6	US-10-953-349-17184	Sequence 17184, A
571	65	5.4	801	6	US-10-953-349-5005	Sequence 5005, Ap	644	64.5	5.4	258	7	US-11-056-355B-22293	Sequence 22293, A
572	65	5.4	802	6	US-10-953-349-5004	Sequence 5004, Ap	645	64.5	5.4	259	7	US-11-371-354-56783	Sequence 56783, A
573	65	5.4	877	7	US-11-056-355B-70310	Sequence 70310, A	646	64.5	5.4	260	6	US-10-953-349-17183	Sequence 17183, A
574	65	5.4	885	7	US-11-056-355B-70309	Sequence 70309, A	647	64.5	5.4	295	7	US-11-434-137-2062	Sequence 2062, Ap
575	65	5.4	895	7	US-11-056-355B-87921	Sequence 87921, A	648	64.5	5.4	295	7	US-11-434-184-2062	Sequence 2062, Ap
576	65	5.4	931	7	US-11-056-355B-70308	Sequence 70308, A	649	64.5	5.4	295	7	US-11-434-203-2062	Sequence 2062, Ap
577	65	5.4	931	7	US-11-056-355B-87920	Sequence 87920, A	650	64.5	5.4	295	7	US-11-434-127-2062	Sequence 2062, Ap
578	65	5.4	937	7	US-11-056-355B-87919	Sequence 87919, A	651	64.5	5.4	299	6	US-10-528-630-15	Sequence 15, Appl
579	64.5	5.4	182	7	US-11-056-355B-42225	Sequence 42225, A	652	64.5	5.4	309	7	US-11-339-553-15	Sequence 15, Appl
580	64.5	5.4	182	7	US-11-056-355B-77363	Sequence 77363, A	653	64.5	5.4	309	7	US-11-073-360-196	Sequence 196, App
581	64.5	5.4	210	7	US-11-056-355B-42223	Sequence 42223, A	654	64.5	5.4	351	7	US-11-371-354-61103	Sequence 61103, A
582	64.5	5.4	210	7	US-11-056-355B-77361	Sequence 77361, A	655	64.5	5.4	363	6	US-10-953-349-22058	Sequence 22058, A
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585	64.5	5.4	238	7	US-11-056-355B-51584	Sequence 51584, A	658	64.5	5.4	411	7	US-11-412-025-18	Sequence 18, Appl
586	64.5	5.4	308	7	US-11-056-355B-51583	Sequence 51583, A	659	64.5	5.4	422	7	US-11-330-403-17833	Sequence 17833, A
587	64.5	5.4	345	7	US-11-056-355B-106594	Sequence 106594,	660	64.5	5.4	431	7	US-11-412-025-20	Sequence 20, Appl
588	64.5	5.4	345	7	US-11-056-355B-117833	Sequence 117833,	661	64.5	5.4	439	7	US-11-056-355B-50481	Sequence 50481, A
589	64.5	5.4	346	7	US-11-056-355B-81937	Sequence 81937, A	662	64.5	5.4	457	7	US-11-330-403-4074	Sequence 4074, Ap
590	64.5	5.4	377	6	US-10-449-902-36418	Sequence 36418, A	663	64.5	5.4	468	7	US-11-056-355B-103246	Sequence 103246,
591	64.5	5.4	389	7	US-11-056-355B-81936	Sequence 81936, A	664	64.5	5.4	468	7	US-11-056-355B-114485	Sequence 114485,
592	64.5	5.4	394	6	US-10-953-349-13165	Sequence 13165, A	665	64.5	5.4	480	7	US-11-056-355B-100298	Sequence 100298,
593	64.5	5.4	398	7	US-11-321-475-4	Sequence 4, Appli	666	64.5	5.4	480	7	US-11-056-355B-111537	Sequence 111537,
594	64.5	5.4	398	7	US-11-330-403-2153	Sequence 2153, Ap	667	64.5	5.4	503	6	US-10-532-868-13	Sequence 13, Appl
595	64.5	5.4	398	7	US-11-330-403-2600	Sequence 2600, Ap	668	64.5	5.4	506	7	US-11-056-355B-50480	Sequence 50480, A
596	64.5	5.4	398	7	US-11-330-403-2800	Sequence 2800, Ap	669	64.5	5.4	512	7	US-11-330-403-12250	Sequence 12250, A
597	64.5	5.4	398	7	US-11-330-403-3862	Sequence 3862, Ap	670	64.5	5.4	535	7	US-11-056-355B-50479	Sequence 50479, A
598	64.5	5.4	398	7	US-11-330-403-5190	Sequence 5190, Ap	671	64.5	5.4	557	7	US-11-056-355B-100297	Sequence 100297,
599	64.5	5.4	398	7	US-11-330-403-9114	Sequence 9114, Ap	672	64.5	5.4	557	7	US-11-056-355B-111536	Sequence 111536,
600	64.5	5.4	398	7	US-11-330-403-11407	Sequence 11407, A	673	64.5	5.4	575	6	US-10-574-398-209	Sequence 209, App
601	64.5	5.4	398	7	US-11-330-403-15565	Sequence 15565, A	674	64.5	5.4	581	6	US-10-807-997-42	Sequence 42, Appl
602	64.5	5.4	398	7	US-11-434-137-4888	Sequence 4888, Ap	675	64.5	5.4	581	7	US-11-256-499A-42	Sequence 42, Appl
603	64.5	5.4	398	7	US-11-434-137-4890	Sequence 4890, Ap	676	64.5	5.4	581	7	US-11-350-375A-42	Sequence 42, Appl
604	64.5	5.4	398	7	US-11-434-184-4888	Sequence 4888, Ap	677	64.5	5.4	586	6	US-10-540-898-558	Sequence 558, App
605	64.5	5.4	398	7	US-11-434-184-4890	Sequence 4890, Ap	678	64.5	5.4	586	6	US-10-574-398-89	Sequence 89, Appl
606	64.5	5.4	398	7	US-11-434-199-4888	Sequence 4888, Ap	679	64.5	5.4	586	7	US-11-371-354-60607	Sequence 60607, A
607	64.5	5.4	398	7	US-11-434-199-4890	Sequence 4890, Ap	680	64.5	5.4	632	7	US-11-056-355B-100296	Sequence 100296,
608	64.5	5.4	398	7	US-11-434-203-4888	Sequence 4888, Ap	681	64.5	5.4	632	7	US-11-056-355B-111535	Sequence 111535,
609	64.5	5.4	398	7	US-11-434-203-4890	Sequence 4890, Ap	682	64.5	5.4	641	7	US-11-493-489-24	Sequence 24, Appl
610	64.5	5.4	398	7	US-11-434-127-4888	Sequence 4888, Ap	683	64.5	5.4	648	7	US-11-493-489-25	Sequence 25, Appl
611	64.5	5.4	398	7	US-11-434-127-4890	Sequence 4890, Ap	684	64.5	5.4	657	7	US-11-493-489-26	Sequence 26, Appl
612	64.5	5.4	400	7	US-11-404-939-491	Sequence 491, App	685	64.5	5.4	661	7	US-11-493-489-2	Sequence 2, Appli

686	64	5.4	661	7	US-11-493-489-27	Sequence 27, Appl	761	63.5	5.3	568	7	US-11-446-871-10	Sequence 10, Appl
687	64	5.4	661	7	US-11-493-489-28	Sequence 28, Appl	762	63.5	5.3	568	7	US-11-446-881-10	Sequence 10, Appl
688	64	5.4	661	7	US-11-493-489-29	Sequence 29, Appl	763	63.5	5.3	605	7	US-11-450-517-69	Sequence 69, Appl
689	64	5.4	675	7	US-11-056-355B-30856	Sequence 30856, A	764	63.5	5.3	619	6	US-10-449-902-31474	Sequence 31474, A
690	64	5.4	675	7	US-11-056-355B-34446	Sequence 34446, A	765	63.5	5.3	672	6	US-10-449-902-52633	Sequence 52633, A
691	64	5.4	688	7	US-11-056-355B-88174	Sequence 88174, A	766	63.5	5.3	678	7	US-11-360-459-193	Sequence 193, App
692	64	5.4	688	7	US-11-056-355B-91930	Sequence 91930, A	767	63.5	5.3	685	7	US-11-330-403-1069	Sequence 1069, App
693	64	5.4	748	7	US-11-056-355B-30855	Sequence 30855, A	768	63.5	5.3	749	7	US-11-371-354-58223	Sequence 58223, A
694	64	5.4	748	7	US-11-056-355B-34445	Sequence 34445, A	769	63.5	5.3	749	7	US-11-371-354-78567	Sequence 78567, A
695	64	5.4	758	7	US-11-293-697-2713	Sequence 2713, Ap	770	63.5	5.3	759	7	US-11-199-853-89	Sequence 89, Appl
696	64	5.4	911	7	US-11-056-355B-73246	Sequence 73246, A	771	63.5	5.3	775	6	US-10-612-783-6844	Sequence 6844, Ap
697	64	5.4	1005	7	US-11-397-222-12	Sequence 12, Appl	772	63.5	5.3	846	6	US-10-449-902-54279	Sequence 54279, A
698	64	5.4	3291	7	US-11-330-403-10065	Sequence 10065, A	773	63.5	5.3	1208	6	US-10-540-898-810	Sequence 810, App
699	63.5	5.3	151	7	US-11-434-137-9022	Sequence 9022, Ap	774	63.5	5.3	1291	7	US-11-090-997-710	Sequence 710, App
700	63.5	5.3	151	7	US-11-434-184-9022	Sequence 9022, Ap	775	63.5	5.3	1348	7	US-11-090-997-704	Sequence 704, App
701	63.5	5.3	151	7	US-11-434-199-9022	Sequence 9022, Ap	776	63.5	5.3	1365	7	US-11-090-997-706	Sequence 706, App
702	63.5	5.3	151	7	US-11-434-203-9022	Sequence 9022, Ap	777	63.5	5.3	1394	6	US-10-953-349-6031	Sequence 6031, Ap
703	63.5	5.3	151	7	US-11-434-127-9022	Sequence 9022, Ap	778	63.5	5.3	1407	6	US-10-953-349-6030	Sequence 6030, Ap
704	63.5	5.3	168	6	US-10-449-902-48466	Sequence 48466, A	779	63.5	5.3	1408	6	US-10-953-349-6029	Sequence 6029, App
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706	63.5	5.3	260	6	US-10-471-571A-4028	Sequence 4028, Ap	781	63.5	5.3	2070	6	US-10-669-920-1225	Sequence 1225, Ap
707	63.5	5.3	265	7	US-11-371-354-62867	Sequence 62867, A	782	63.5	5.3	2076	7	US-11-090-997-700	Sequence 700, App
708	63.5	5.3	285	7	US-11-371-354-77419	Sequence 77419, A	783	63.5	5.3	2080	7	US-11-090-997-1066	Sequence 1066, Ap
709	63.5	5.3	313	6	US-10-953-349-23774	Sequence 23774, A	784	63	5.3	52	7	US-11-478-144-557	Sequence 557, App
710	63.5	5.3	313	7	US-11-056-355B-59946	Sequence 59946, A	785	63	5.3	75	7	US-11-199-489A-110	Sequence 110, App
711	63.5	5.3	325	6	US-10-669-920-237	Sequence 237, App	786	63	5.3	146	7	US-11-056-355B-20547	Sequence 20547, A
712	63.5	5.3	334	6	US-10-953-349-23773	Sequence 2373, App	787	63	5.3	199	7	US-11-056-355B-4425	Sequence 4425, Ap
713	63.5	5.3	334	7	US-11-056-355B-59945	Sequence 59945, A	788	63	5.3	200	7	US-11-330-403-3581	Sequence 3581, Ap
714	63.5	5.3	362	7	US-11-197-712-2871	Sequence 280, App	789	63	5.3	239	7	US-11-371-354-74019	Sequence 74019, A
715	63.5	5.3	365	6	US-10-953-349-2271	Sequence 2271, Ap	790	63	5.3	259	7	US-11-283-567-3	Sequence 3, Appl1
716	63.5	5.3	365	7	US-11-056-355B-40033	Sequence 40033, A	791	63	5.3	259	7	US-11-268-745-40	Sequence 40, Appl
717	63.5	5.3	370	6	US-10-669-920-239	Sequence 239, App	792	63	5.3	260	7	US-11-090-997-432	Sequence 432, App
718	63.5	5.3	389	7	US-11-330-403-5502	Sequence 5502, Ap	793	63	5.3	261	6	US-10-669-920-982	Sequence 982, App
719	63.5	5.3	392	7	US-11-366-965-26	Sequence 26, Appl	794	63	5.3	271	6	US-10-953-349-12538	Sequence 12538, A
720	63.5	5.3	400	7	US-11-330-403-6060	Sequence 6060, Ap	795	63	5.3	309	7	US-11-358-841-13	Sequence 13, Appl
721	63.5	5.3	402	7	US-11-199-489A-46	Sequence 46, Appl	796	63	5.3	310	6	US-10-953-349-6642	Sequence 6642, Ap
722	63.5	5.3	423	6	US-10-953-349-2270	Sequence 2270, Ap	797	63	5.3	310	7	US-11-056-355B-23422	Sequence 23422, A
723	63.5	5.3	423	7	US-11-056-355B-40032	Sequence 40032, A	798	63	5.3	311	7	US-11-056-355B-25644	Sequence 25644, A
724	63.5	5.3	425	6	US-10-449-902-29720	Sequence 29720, A	799	63	5.3	311	6	US-10-953-349-12537	Sequence 12537, A
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726	63.5	5.3	426	7	US-11-330-403-10234	Sequence 10234, A	801	63	5.3	319	7	US-11-358-841-12	Sequence 12, Appl
727	63.5	5.3	428	7	US-11-412-025-36	Sequence 36, Appl	802	63	5.3	332	7	US-11-056-355B-71005	Sequence 71005, A
728	63.5	5.3	433	7	US-11-056-355B-43312	Sequence 43312, A	803	63	5.3	332	7	US-11-056-355B-73873	Sequence 73873, A
729	63.5	5.3	437	7	US-11-056-355B-40573	Sequence 40573, A	804	63	5.3	333	7	US-11-056-355B-84881	Sequence 84881, A
730	63.5	5.3	437	7	US-11-056-355B-76831	Sequence 76831, A	805	63	5.3	339	6	Sequence 5006, Ap	
731	63.5	5.3	437	7	US-11-056-355B-103986	Sequence 103986, A	806	63	5.3	341	7	Sequence 106029, A	
732	63.5	5.3	437	7	US-11-056-355B-115225	Sequence 115225, A	807	63	5.3	341	7	Sequence 117268, A	
733	63.5	5.3	438	7	US-11-056-355B-71678	Sequence 71678, A	808	63	5.3	350	7	Sequence 84880, A	
734	63.5	5.3	443	7	US-11-434-137-6676	Sequence 6676, Ap	809	63	5.3	350	7	Sequence 59269, A	
735	63.5	5.3	443	7	US-11-434-184-6676	Sequence 6676, Ap	810	63	5.3	351	7	Sequence 71004, A	
736	63.5	5.3	443	7	US-11-434-199-6676	Sequence 6676, Ap	811	63	5.3	351	7	Sequence 73872, A	
737	63.5	5.3	443	7	US-11-434-203-6676	Sequence 6676, Ap	812	63	5.3	358	6	Sequence 35482, A	
738	63.5	5.3	443	7	US-11-434-127-6676	Sequence 6676, Ap	813	63	5.3	358	7	Sequence 84879, A	
739	63.5	5.3	447	7	US-11-056-355B-40572	Sequence 40572, A	814	63	5.3	358	7	Sequence 106028, A	
740	63.5	5.3	447	7	US-11-056-355B-76830	Sequence 76830, A	815	63	5.3	358	7	Sequence 117267, A	
741	63.5	5.3	447	7	US-11-056-355B-103985	Sequence 103985, A	816	63	5.3	361	7	Sequence 106027, A	
742	63.5	5.3	447	7	US-11-056-355B-115224	Sequence 115224, A	817	63	5.3	361	7	Sequence 117266, A	
743	63.5	5.3	450	7	US-11-056-355B-71027	Sequence 71027, A	818	63	5.3	371	6	Sequence 3551, Ap	
744	63.5	5.3	463	7	US-11-056-355B-40571	Sequence 40571, A	819	63	5.3	375	7	Sequence 10, Appl	
745	63.5	5.3	463	7	US-11-056-355B-76829	Sequence 76829, A	820	63	5.3	407	7	Sequence 4486, Ap	
746	63.5	5.3	463	7	US-11-056-355B-103984	Sequence 103984, A	821	63	5.3	410	7	Sequence 9, Appl1	
747	63.5	5.3	463	7	US-11-056-355B-115223	Sequence 115223, A	822	63	5.3	415	7	Sequence 22, Appl	
748	63.5	5.3	463	7	US-11-330-403-10251	Sequence 10251, A	823	63	5.3	415	7	Sequence 73871, A	
749	63.5	5.3	468	7	US-11-330-403-16953	Sequence 16953, A	824	63	5.3	422	7	Sequence 104980, A	
750	63.5	5.3	468	7	US-11-371-354-62463	Sequence 62463, A	825	63	5.3	432	7	Sequence 116219, A	
751	63.5	5.3	487	6	US-10-552-156-171	Sequence 171, App	826	63	5.3	432	7	Sequence 82528, A	
754	63.5	5.3	489	7	US-11-371-354-55053	Sequence 55053, A	827	63	5.3	438	7	Sequence 69665, A	
755	63.5	5.3	511	7	US-11-056-355B-71677	Sequence 71677, A	828	63	5.3	446	7	Sequence 4485, Ap	
756	63.5	5.3	545	6	US-10-612-783-6688	Sequence 6688, Ap	829	63	5.3	451	7	Sequence 71003, A	
757	63.5	5.3	555	7	US-11-056-355B-71676	Sequence 71676, A	830	63	5.3	451	6	Sequence 568, App	
758	63.5	5.3	568	7	US-11-233-089-2	Sequence 2, Appl1	831	63	5.3	458	7	Sequence 69664, A	
759	63.5	5.3	568	7	US-11-233-089-4	Sequence 4, Appl1	832	63	5.3	462	7	Sequence 12, Appl	
760	63.5	5.3	568	7	US-11-446-854-10	Sequence 10, Appl	833	63	5.3	469	6	Sequence 12, Appl	

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845	63	5.3	532	7	US-11-434-184-2538	Sequence 2538, Ap	920	62.5	5.2	360	7	US-11-434-203-9142	Sequence 9142, Ap
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851	63	5.3	541	7	US-11-056-355B-41123	Sequence 41123, A	926	62.5	5.2	367	7	US-11-434-184-214	Sequence 214, App
852	63	5.3	541	7	US-11-056-355B-47701	Sequence 47701, A	927	62.5	5.2	367	7	US-11-434-199-214	Sequence 214, App
853	63	5.3	541	7	US-11-056-355B-104978	Sequence 104978, A	928	62.5	5.2	367	7	US-11-434-203-214	Sequence 214, App
854	63	5.3	541	7	US-11-056-355B-116217	Sequence 116217, A	929	62.5	5.2	367	7	US-11-434-127-214	Sequence 214, App
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863	63	5.3	616	7	US-11-371-354-62121	Sequence 62121, A	938	62.5	5.2	413	6	US-10-953-349-26620	Sequence 26620, A
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869	63	5.3	629	7	US-11-434-137-8922	Sequence 8922, Ap	944	62.5	5.2	439	7	US-11-056-355B-57376	Sequence 57376, A
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871	63	5.3	629	7	US-11-434-199-8922	Sequence 8922, Ap	946	62.5	5.2	442	6	US-10-574-398-339	Sequence 339, App
872	63	5.3	629	7	US-11-434-203-8922	Sequence 8922, Ap	947	62.5	5.2	442	7	US-11-404-939-497	Sequence 497, App
873	63	5.3	629	7	US-11-434-127-8922	Sequence 8922, Ap	948	62.5	5.2	442	7	US-11-090-997-1108	Sequence 1108, Ap
874	63	5.3	648	7	US-11-434-137-5802	Sequence 5802, Ap	949	62.5	5.2	442	7	US-11-371-354-60297	Sequence 60297, A
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885	63	5.3	950	6	US-10-449-902-41479	Sequence 41479, A	960	62.5	5.2	504	7	US-11-293-697-2761	Sequence 2761, Ap
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887	63	5.3	1028	6	US-10-449-902-42278	Sequence 42278, A	962	62.5	5.2	507	7	US-11-330-403-11763	Sequence 11763, A
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889	63	5.3	1181	7	US-11-241-596-256	Sequence 256, App	964	62.5	5.2	539	7	US-11-371-354-61765	Sequence 61765, A
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891	63	5.3	1181	7	US-11-241-596-258	Sequence 258, App	966	62.5	5.2	578	6	US-10-533-519-963	Sequence 963, App
892	63	5.3	3668	7	US-11-357-566-4	Sequence 4, Appli	967	62.5	5.2	578	7	US-11-371-354-56767	Sequence 56767, A
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999	62	5.2	220	7	US-11-434-127-8536	Sequence 8536, Ap	1072	62	5.2	485	6	US-10-536-935A-6	Sequence 6, Appl
1000	62	5.2	237	6	US-10-471-571A-1910	Sequence 1910, Ap	1073	62	5.2	485	7	US-11-409-453-6	Sequence 6, Appl
1001	62	5.2	244	7	US-11-371-354-73313	Sequence 73313, A	1074	62	5.2	485	7	US-11-409-530-6	Sequence 6, Appl
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1005	62	5.2	258	6	US-10-449-902-45635	Sequence 45635, A	1078	62	5.2	514	7	US-11-296-657-22	Sequence 22, Appl
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1024	62	5.2	272	7	US-11-251-466-22	Sequence 22, Appl	1097	62	5.2	764	7	US-11-056-355B-71563	Sequence 71563, A
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1031	62	5.2	303	7	US-11-357-566-23	Sequence 23, Appl	1105	62	5.2	1715	6	US-10-502-394-93	Sequence 93, Appl
1032	62	5.2	312	7	US-11-140-450-55	Sequence 55, Appl	1106	62	5.2	1762	6	US-10-502-394-94	Sequence 94, Appl
1033	62	5.2	312	7	US-11-140-450-58	Sequence 58, Appl	1107	62	5.2	1762	6	US-10-502-394-94	Sequence 94, Appl
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1035	62	5.2	322	6	US-10-449-902-29886	Sequence 29886, A	1109	62	5.2	1777	6	US-10-570-909-17	Sequence 17, Appl
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1037	62	5.2	330	7	US-11-434-184-9560	Sequence 9560, Ap	1111	62	5.2	1780	7	US-11-107-336-74	Sequence 74, Appl
1038	62	5.2	330	7	US-11-434-199-9560	Sequence 9560, Ap	1112	62	5.2	3011	7	US-11-254-252-20	Sequence 20, Appl
1039	62	5.2	330	7	US-11-434-203-9560	Sequence 9560, Ap	1113	62	5.2	3515	6	US-10-526-572-12	Sequence 12, Appl
1040	62	5.2	330	7	US-11-434-127-9560	Sequence 9560, Ap	1114	61.5	5.1	107	7	US-11-305-666-78	Sequence 78, Appl
1041	62	5.2	340	7	US-11-056-355B-47620	Sequence 47620, A	1115	61.5	5.1	163	7	US-11-090-997-194	Sequence 194, Appl
1042	62	5.2	344	7	US-10-953-349-23477	Sequence 23477, A	1116	61.5	5.1	173	7	US-11-056-355B-61596	Sequence 61596, A
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1046	62	5.2	355	7	US-11-434-184-5228	Sequence 5228, Ap	1120	61.5	5.1	177	7	US-11-434-203-7070	Sequence 7070, Ap
1047	62	5.2	355	7	US-11-434-199-5228	Sequence 5228, Ap	1121	61.5	5.1	177	7	US-11-434-199-7070	Sequence 7070, Ap
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1052	62	5.2	360	7	US-11-371-354-67277	Sequence 67277, A	1126	61.5	5.1	240	7	US-11-434-137-1828	Sequence 1828, Ap
1053	62	5.2	392	6	US-10-953-349-10746	Sequence 10746, A	1127	61.5	5.1	240	7	US-11-434-184-1828	Sequence 1828, Ap
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1132	61.5	5.1	282	7	US-11-305-666-63	Sequence 63, Appl	1205	61.5	5.1	557	6	US-10-449-902-49568	Sequence 49568, A
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1134	61.5	5.1	286	7	US-11-305-666-66	Sequence 66, Appl	1207	61.5	5.1	593	6	US-10-552-156-306	Sequence 306, App
1135	61.5	5.1	286	7	US-11-305-666-84	Sequence 84, Appl	1208	61.5	5.1	610	6	US-10-449-902-53952	Sequence 53952, A
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1141	61.5	5.1	330	7	US-11-434-137-9734	Sequence 9734, Ap	1214	61.5	5.1	659	6	US-10-552-156-307	Sequence 307, App
1142	61.5	5.1	330	7	US-11-434-184-9498	Sequence 9498, Ap	1215	61.5	5.1	659	6	US-10-552-156-309	Sequence 309, App
1143	61.5	5.1	330	7	US-11-434-184-9734	Sequence 9734, Ap	1216	61.5	5.1	659	6	US-10-552-156-310	Sequence 310, App
1144	61.5	5.1	330	7	US-11-434-199-9498	Sequence 9498, Ap	1217	61.5	5.1	674	6	US-10-533-519-910	Sequence 910, App
1145	61.5	5.1	330	7	US-11-434-199-9734	Sequence 9734, Ap	1218	61.5	5.1	678	7	US-11-289-102-320	Sequence 320, App
1146	61.5	5.1	330	7	US-11-434-203-9498	Sequence 9498, Ap	1219	61.5	5.1	685	7	US-11-056-355B-100222	Sequence 100222, A
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1164	61.5	5.1	380	6	US-10-513-024-330	Sequence 302, App	1237	61.5	5.1	965	7	US-11-178-560-3	Sequence 3, Appli
1165	61.5	5.1	380	7	US-11-434-137-502	Sequence 502, App	1238	61.5	5.1	965	7	US-11-409-323-3	Sequence 3, Appli
1166	61.5	5.1	380	7	US-11-434-137-504	Sequence 504, App	1239	61.5	5.1	1018	6	US-10-449-902-41063	Sequence 41063, A
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1168	61.5	5.1	380	7	US-11-434-137-7072	Sequence 7072, Ap	1241	61.5	5.1	1514	7	US-11-056-355B-39531	Sequence 39531, A
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1171	61.5	5.1	380	7	US-11-434-184-504	Sequence 504, App	1244	61.5	5.1	1514	7	US-10-533-519-572	Sequence 572, App
1172	61.5	5.1	380	7	US-11-434-184-1036	Sequence 1036, Ap	1245	61.5	5.1	2000	6	US-10-538-002-127	Sequence 127, App
1173	61.5	5.1	380	7	US-11-434-184-7072	Sequence 7072, Ap	1246	61.5	5.1	2306	6	US-10-538-002-174	Sequence 174, App
1174	61.5	5.1	380	7	US-11-434-184-9068	Sequence 9068, Ap	1247	61.5	5.1	3458	7	US-10-822-303-9914	Sequence 9914, App
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1181	61.5	5.1	380	7	US-11-434-203-504	Sequence 504, App	1254	61.5	5.1	207	7	US-11-434-199-9874	Sequence 9874, Ap
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1186	61.5	5.1	380	7	US-11-434-127-504	Sequence 504, App	1259	61.5	5.1	212	7	US-11-434-184-2812	Sequence 2812, Ap
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1198	61.5	5.1	468	7	US-11-056-355B-37595	Sequence 37595, A	1271	61.5	5.1	256	6	US-10-623-808-6	Sequence 6, Appli
1199	61.5	5.1	468	7	US-11-056-355B-42155	Sequence 42155, A	1272	61.5	5.1	256	7	US-11-128-423-6	Sequence 6, Appli
1200	61.5	5.1	469	7	US-11-371-354-12239	Sequence 12239, A	1273	61.5	5.1	276	7	US-11-370-754-5	Sequence 5, Appli
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1276	61	5.1	288	7	US-11-056-355B-59223	Sequence 59223, A	1349	61	5.1	1079	6	US-10-449-902-41149	Sequence 41149, A
1277	61	5.1	289	6	US-10-805-394-5753	Sequence 5753, Ap	1350	61	5.1	1279	6	US-11-049-902-53619	Sequence 53619, A
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1280	61	5.1	299	7	US-11-073-360-195	Sequence 195, App	1353	61	5.1	1471	7	US-11-056-355B-84133	Sequence 84133, A
1281	61	5.1	301	6	US-10-449-902-55919	Sequence 55919, A	1354	61	5.1	1487	7	US-11-056-355B-84132	Sequence 84132, A
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1284	61	5.1	312	7	US-11-140-450-59	Sequence 59, Appl	1357	61	5.1	1913	7	US-11-063-439-163	Sequence 163, App
1285	61	5.1	313	7	US-11-371-354-66917	Sequence 66917, A	1358	61	5.1	1954	7	US-11-090-997-1036	Sequence 1036, Ap
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1287	61	5.1	324	6	US-10-562-463-16	Sequence 16, Appl	1360	61	5.1	2530	7	US-11-046-560A-23	Sequence 23, Appl
1288	61	5.1	324	7	US-11-056-355B-103484	Sequence 103484, A	1361	61	5.1	3011	6	US-10-520-153-14	Sequence 14, Appl
1289	61	5.1	324	7	US-11-056-355B-114723	Sequence 114723, A	1362	61	5.1	3011	6	US-10-527-422-16	Sequence 16, Appl
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1291	61	5.1	332	7	US-11-056-355B-38710	Sequence 38710, A	1364	61	5.1	3011	7	US-11-236-836-14	Sequence 14, Appl
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1293	61	5.1	338	7	US-11-056-355B-59222	Sequence 59222, A	1366	61	5.1	3011	7	US-11-411-493-1	Sequence 1, Appl
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1296	61	5.1	347	7	US-11-056-355B-114722	Sequence 114722, A	1369	61	5.1	3222	7	US-11-063-439-137	Sequence 137, App
1297	61	5.1	363	7	US-11-056-355B-38708	Sequence 38708, A	1370	61	5.1	3469	7	US-11-063-439-106	Sequence 106, App
1298	61	5.1	377	6	US-10-953-349-12021	Sequence 12021, A	1371	61	5.1	3473	7	US-11-063-439-199	Sequence 199, App
1299	61	5.1	392	7	US-11-056-355B-103482	Sequence 103482, A	1372	61	5.1	3490	7	US-11-063-439-126	Sequence 126, App
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1301	61	5.1	398	7	US-11-330-403-13236	Sequence 13236, A	1374	61	5.1	3497	7	US-11-063-439-172	Sequence 172, App
1302	61	5.1	407	7	US-11-366-965-273	Sequence 273, App	1375	61	5.1	3499	7	US-11-063-439-116	Sequence 116, App
1303	61	5.1	414	6	US-10-805-394-6146	Sequence 6146, Ap	1376	61	5.1	3507	7	US-11-063-439-196	Sequence 196, App
1304	61	5.1	417	7	US-11-056-355B-77908	Sequence 77908, A	1377	61	5.1	3508	7	US-11-063-439-166	Sequence 166, App
1305	61	5.1	421	7	US-11-056-355B-97221	Sequence 97221, A	1378	61	5.1	3508	7	US-11-063-439-168	Sequence 168, App
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OM protein - protein search, using sw model

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(without alignments)
577.301 Million cell updates/sec

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Perfect score: 1195
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Total number of hits satisfying chosen parameters: 283416

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

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1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	664	55.6	445	2 I38027	MLN 64 protein - h
2	204	17.1	478	2 T16170	hypothetical prote
3	102.5	8.6	348	2 H90281	hypothetical prote
4	93.5	7.8	424	2 D75080	glucose-1-phosphat
5	90	7.5	1911	2 T43048	calcium channel al
6	86.5	7.2	767	2 T21969	hypothetical prote
7	85.5	7.2	396	2 B81299	probable molybdopt
8	85.5	7.2	438	2 A57219	Batten disease-rel
9	85	7.1	448	2 G70172	conserved hypotet
10	84.5	7.1	471	2 A41680	integral membrane
11	83.5	7.0	352	2 H97002	probable integral
12	83	6.9	291	2 AE0302	sugar ABC transpor
13	83	6.9	590	1 S34960	NADH2 dehydrogenas
14	82.5	6.9	186	2 B29835	Tras protein - Esc
15	82.5	6.9	239	1 C64227	hypothetical prote
16	82.5	6.9	341	2 S51265	probable N-acetylgl
17	82.5	6.9	406	2 T43120	conserved hypotet
18	82.5	6.9	891	2 T37397	major core protein
19	82	6.9	589	2 T52070	RNAL protein homol
20	82	6.9	589	2 A36983	RNAL homolog fucl
21	82	6.9	1466	2 T30566	ATP-binding casset
22	81	6.8	385	2 B84447	hypothetical prote
23	81	6.8	529	2 T23190	hypothetical prote
24	81	6.8	532	2 S46831	probable membrane
25	80.5	6.7	156	2 I84498	melatonin receptor
26	80.5	6.7	322	2 T45568	hypothetical prote
27	80.5	6.7	396	2 T50229	probable transmemb
28	80.5	6.7	417	2 C44038	tryptophan permeas
29	80.5	6.7	463	2 AE1155	amino acid transpo

probable integral
membrane
membrane protein t
major core protein
major core protein
probable glucan sy
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hypothetical prote
RTM1 protein - yea
hypothetical prote
probable SNF2 subf
amino acid transpo
immediate-early pr
hypothetical prote
spermidine/putresc
rnfD protein homol
serotonin receptor
IB3/5-polypeptide
cdd2 protein - Clo
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probable sugar ABC
hypothetical prote
probable membrane
potassium channel
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hypothetical prote
low affinity trypt
low affinity trypt
tryptophan transpo
5-hydroxytryptamin
NADH2 dehydrogenas

103	75.5	6.3	593	2	H64594	multidrug resistant	176	72.5	6.1	325	2	H86670	hypothetical prote
104	75.5	6.3	708	2	T29669	hypothetical prote	177	72.5	6.1	336	2	C98951	protein C38C3.2 [i
105	75.5	6.3	178	2	T52107	anion channel prot	178	72.5	6.1	389	2	A55493	oxytocin receptor
106	75.5	6.3	1142	2	T39103	probable negative	179	72.5	6.1	428	2	AF0173	probable parquat-
107	75	6.3	249	2	G64470	sulfate/thiosulfat	180	72.5	6.1	499	2	H70453	virulence factor M
108	75	6.3	274	2	A82509	probable phosphat	181	72.5	6.1	513	2	S47631	pituitary adenylat
109	75	6.3	330	2	B71163	probable oligopept	182	72.5	6.1	522	2	T29705	hypothetical prote
110	75	6.3	473	2	A38627	gamma-aminobutyric	183	72.5	6.1	635	2	T23485	hypothetical prote
111	75	6.3	526	2	T45850	hypothetical prote	184	72.5	6.1	718	2	SS7913	probable transloc
112	75	6.3	649	2	C69810	anion-binding prot	185	72.5	6.1	749	2	C84508	probable cap-bind
113	75	6.3	753	2	H90124	hypothetical prote	186	72.5	6.1	1539	2	T30037	hypothetical prote
114	75	6.3	248	1	D42088	adenylate cyclase	187	72	6.0	279	2	T21099	hypothetical prote
115	74.5	6.2	276	2	A95881	probable trehalose	188	72	6.0	306	2	AE1156	hypothetical prote
116	74.5	6.2	335	2	H72420	oligopeptide ABC t	189	72	6.0	339	2	G97139	probable permease
117	74.5	6.2	355	2	JC4304	orphan G protein-c	190	72	6.0	377	2	T27805	hypothetical prote
118	74.5	6.2	471	2	A34863	serotonin receptor	191	72	6.0	379	2	T11349	ubiquinol-cytochro
119	74.5	6.2	473	2	B84143	Na+/H+ antiporter	192	72	6.0	415	1	WNAD52	late L1 52K protei
120	74.5	6.2	500	2	T14826	transcription init	193	72	6.0	415	1	WNAD65	late L1 52K protei
121	74.5	6.2	574	2	T05964	probable low-affin	194	72	6.0	453	2	T39155	glycosyl hydrolase
122	74.5	6.2	618	1	S38004	probable transport	195	72	6.0	453	2	D89760	conserved hypothet
123	74.5	6.2	1808	2	T47792	hypothetical prote	196	72	6.0	479	2	S64587	hypothetical prote
124	74	6.2	231	1	C69540	cobalamin (5'-phos	197	72	6.0	497	2	G96611	probable cytochrom
125	74	6.2	231	1	B69422	quinone-reactive N	198	72	6.0	514	2	T15338	hypothetical prote
126	74	6.2	281	1	S25018	NAOH2 dehydrogen	199	72	6.0	594	2	T42660	hypothetical prote
127	74	6.2	286	2	S73424	spermidine/puoresc	200	72	6.0	600	2	T39873	hypothetical prote
128	74	6.2	312	2	C72547	probable aspartate	201	72	6.0	630	2	T07966	probable ethylene
129	74	6.2	312	2	H86732	hypothetical prote	202	72	6.0	1038	2	S37854	hypothetical prote
130	74	6.2	349	2	JC6311	interferon recepto	203	72	6.0	1094	2	S22573	DNA-directed DNA p
131	74	6.2	350	2	I38848	Mel-1a melatonin r	204	72	6.0	1113	2	T20140	hypothetical prote
132	74	6.2	396	2	H89869	hypothetical prote	205	72	6.0	1220	2	T18291	hypothetical prote
133	74	6.2	442	2	C86859	transmembrane efl	206	72	6.0	1275	2	JU0092	patched protein -
134	74	6.2	449	2	S02011	serotonin receptor	207	72	6.0	1282	2	T30804	trp protein - frui
135	74	6.2	475	2	T36137	probable amino aci	208	71.5	6.0	210	2	S52050	p-glycoprotein 6 -
136	74	6.2	485	2	T24115	cytochrome P450 d1	209	71.5	6.0	225	1	MMIH68	cytochrome-c oxida
137	74	6.2	487	1	C71417	hypothetical prote	210	71.5	6.0	237	1	H70975	E1 membrane glycop
138	74	6.2	493	2	JC7378	L-lysine 6-aminor	211	71.5	6.0	246	2	AG3644	hypothetical prote
139	74	6.2	1123	2	T51517	telomerase reverse	212	71.5	6.0	301	2	F86647	flagellar biosynth
140	73.5	6.2	153	2	E95845	conserved hypothet	213	71.5	6.0	341	2	F90084	hypothetical prote
141	73.5	6.2	192	2	A84727	hypothetical prote	214	71.5	6.0	345	2	T33706	hypothetical prote
142	73.5	6.2	216	2	G70474	hypothetical prote	215	71.5	6.0	348	2	D82252	RnfD-related prote
143	73.5	6.2	318	2	S76713	hypothetical prote	216	71.5	6.0	355	2	AB3516	hypothetical prote
144	73.5	6.2	338	2	I40448	conserved hypothet	217	71.5	6.0	362	2	S48689	sensory transducti
145	73.5	6.2	379	2	S58448	ubiquinol-cytochro	218	71.5	6.0	366	2	S51280	prostaglandin E(2)
146	73.5	6.2	384	2	AF0636	glucans biosynthes	219	71.5	6.0	366	2	I46469	Ep3-alpha receptor
147	73.5	6.2	385	1	S01511	ubiquinol-cytochro	220	71.5	6.0	381	2	T11776	Mel-1a melatonin r
148	73.5	6.2	385	1	A69804	ABC transporter (A	221	71.5	6.0	383	2	T38194	ubiquinol-cytochro
149	73.5	6.2	413	2	AD1738	Similar to multiar	222	71.5	6.0	386	1	S34043	hypothetical prote
150	73.5	6.2	442	2	C96672	hypothetical prote	223	71.5	6.0	390	2	S66497	oxytocin receptor
151	73.5	6.2	491	1	ED8EM5	immediate-early pr	224	71.5	6.0	435	2	AD1340	isotocin receptor
152	73.5	6.2	634	2	F82623	potassium uptake p	225	71.5	6.0	435	2	AB1711	maltodextrin ABC-t
153	73.5	6.2	637	2	H83945	DNA mismatch repai	226	71.5	6.0	471	2	PS0154	maltodextrin ABC-t
154	73.5	6.2	637	2	H83945	hypothetical prote	227	71.5	6.0	510	2	T10124	hexose transport p
155	73.5	6.2	731	2	T31914	hypothetical prote	228	71.5	6.0	524	2	T02499	hypothetical prote
156	73.5	6.2	1095	2	E96744	probable oligopept	229	71.5	6.0	603	2	H90061	hypothetical prote
157	73.5	6.2	1174	2	A39927	RNA-directed RNA p	230	71.5	6.0	651	2	T46050	hypothetical prote
158	73	6.1	114	2	F71925	cag island protein	231	71.5	6.0	669	2	D64137	betT protein homol
159	73	6.1	282	2	S26030	NAOH2 dehydrogen	232	71.5	6.0	670	2	A49580	mediates transport
160	73	6.1	339	1	T15560	hypothetical prote	233	71.5	6.0	823	2	T34472	hypothetical prote
161	73	6.1	450	1	WZBE84	49-2K membrane pr	234	71.5	6.0	1407	2	B42239	adenylate cyclase
162	73	6.1	453	2	T30985	hypothetical prote	235	71.5	6.0	3010	1	S18030	genome polyprotein
163	73	6.1	553	2	A71823	hypothetical prote	236	71	5.9	114	2	H64586	cag pathogenicity
164	73	6.1	788	2	G89901	hypothetical prote	237	71	5.9	225	1	MMIHAI	E1 membrane glycop
165	73	6.1	971	2	T00268	hypothetical prote	238	71	5.9	250	2	A82367	conserved hypothet
166	73	6.1	1075	2	B96508	hypothetical prote	239	71	5.9	258	2	A81355	probable processin
167	73	6.1	6805	2	S20901	titin - rabbit (fr	240	71	5.9	290	2	S33443	chlorophyll a/b-bi
168	72.5	6.1	209	2	S73929	hypothetical prote	241	71	5.9	339	2	T16745	hypothetical prote
169	72.5	6.1	222	2	B85866	probable transport	242	71	5.9	345	2	T12372	NAOH2 dehydrogen
170	72.5	6.1	222	2	B91022	probable transport	243	71	5.9	345	2	T25561	hypothetical prote
171	72.5	6.1	222	2	H64996	hypothetical prote	244	71	5.9	361	2	C90603	hypothetical prote
172	72.5	6.1	255	2	A60944	ubiquinol-cytochro	245	71	5.9	391	2	F86759	hypothetical prote
173	72.5	6.1	291	2	T02986	chlorophyll a/b-bi	246	71	5.9	416	2	E87286	3-deoxy-D-manno-oc
174	72.5	6.1	307	2	A86696	conserved hypothet	247	71	5.9	423	2	AF1335	transcription regu
175	72.5	6.1	315	2	H95598	protein F20N2.8 [i	248	71	5.9	471	2	A43956	serotonin receptor

249	71	5.9	546	2	S48932	hypothetical prote	322	69.5	5.8	285	2	F70194	hypothetical prote
250	71	5.9	563	2	T38766	probable transcrip	323	69.5	5.8	321	2	S59388	probable membrane
251	71	5.9	576	2	T22509	hypothetical prote	324	69.5	5.8	339	2	A97736	hypothetical prote
252	71	5.9	620	2	A58932	cytochrome C-type	325	69.5	5.8	347	2	G90444	hypothetical prote
253	71	5.9	676	2	E96725	hypothetical prote	326	69.5	5.8	361	2	S58186	probable G protein
254	71	5.9	788	2	E71813	probable component	327	69.5	5.8	354	2	A53216	prostaglandin E2 r
255	71	5.9	913	2	T52485	neurofilament prot	328	69.5	5.8	362	2	S36766	prostaglandin E re
256	71	5.9	2437	2	T18482	hypothetical prote	329	69.5	5.8	384	2	S62758	ubiquinol-cytochro
257	70.5	5.9	203	1	T31684	probable bacitraci	330	69.5	5.8	385	2	S36765	prostaglandin E re
258	70.5	5.9	266	2	H98208	probable permease	331	69.5	5.8	387	2	S36767	prostaglandin E re
259	70.5	5.9	286	2	A13077	hypothetical prote	332	69.5	5.8	394	2	T32561	hypothetical prote
260	70.5	5.9	266	2	T41414	probable receptor-	333	69.5	5.8	400	2	AG1208	cell-division prot
261	70.5	5.9	279	2	AH2408	permease protein o	334	69.5	5.8	402	2	S51791	Drosophila translo
262	70.5	5.9	291	2	S22041	hypothetical prote	335	69.5	5.8	405	2	E90986	probable colanic a
263	70.5	5.9	340	2	S76294	hypothetical prote	336	69.5	5.8	405	2	H85831	probable colanic a
264	70.5	5.9	352	2	B90537	hypothetical prote	337	69.5	5.8	405	2	G64971	Putative colanic a
265	70.5	5.9	365	2	I38748	prostaglandin recep	338	69.5	5.8	411	2	B53216	prostaglandin E2 r
266	70.5	5.9	365	2	S13115	prostaglandin E re	339	69.5	5.8	417	2	S36764	prostaglandin E re
267	70.5	5.9	374	2	I38747	prostaglandin recep	340	69.5	5.8	421	2	G72300	conserved hypothet
268	70.5	5.9	374	2	S51317	prostaglandin E re	341	69.5	5.8	436	2	T44832	probable emulsan r
269	70.5	5.9	388	2	S51316	prostaglandin E re	342	69.5	5.8	453	2	D98003	conserved hypothet
270	70.5	5.9	388	2	I38750	prostaglandin recep	343	69.5	5.8	477	2	T25798	hypothetical prote
271	70.5	5.9	389	2	S71336	mesotocin receptor	344	69.5	5.8	490	2	E82740	C4-dicarboxylate t
272	70.5	5.9	390	2	S43375	prostaglandin E re	345	69.5	5.8	503	2	C86250	hypothetical prote
273	70.5	5.9	390	2	S51313	prostaglandin E re	346	69.5	5.8	507	2	T50054	probable transport
274	70.5	5.9	393	2	S51318	prostaglandin E re	347	69.5	5.8	515	2	E86534	ADP/ATP translocas
275	70.5	5.9	423	1	E71065	hypothetical prote	348	69.5	5.8	515	2	G86581	integral membrane
276	70.5	5.9	425	2	S51319	prostaglandin E re	349	69.5	5.8	547	2	T72042	integral membrane
277	70.5	5.9	472	2	AG3600	cellulose synthase	350	69.5	5.8	557	2	JW0089	organic cation tra
278	70.5	5.9	496	2	B64638	conserved hypothet	351	69.5	5.8	557	2	AC2137	ABC transporter At
279	70.5	5.9	521	2	B64181	probable cytochrom	352	69.5	5.8	570	2	B96776	hypothetical prote
280	70.5	5.9	548	2	A81650	conserved hypothet	353	69.5	5.8	577	2	D97337	mismatch repair pr
281	70.5	5.9	556	2	T16790	hypothetical prote	354	69.5	5.8	579	2	AG1412	DNA polymerase III
282	70.5	5.9	574	2	S45754	probable membrane	355	69.5	5.8	579	2	AF1788	gamma-aminobutyric
283	70.5	5.9	598	2	F46027	gamma-aminobutyric	356	69.5	5.8	599	2	S11073	hypothetical prote
284	70.5	5.9	599	1	ACRTGT	gamma-aminobutyric	357	69.5	5.8	604	2	T31042	hypothetical prote
285	70.5	5.9	700	2	T10566	probable serine/th	358	69.5	5.8	607	2	F84525	Mutator-like trans
286	70.5	5.9	766	2	T48463	hypothetical prote	359	69.5	5.8	616	2	E84463	Mutator-like trans
287	70.5	5.9	1026	2	T18220	chitin synthase (E	360	69.5	5.8	877	2	S58824	probable membrane
288	70.5	5.9	1583	2	F97846	hypothetical prote	361	69.5	5.8	881	2	S46633	probable membrane
289	70.5	5.9	1787	2	T20160	hypothetical prote	362	69.5	5.8	1704	2	S71363	probable ATP-bindi
290	70.5	5.9	5138	2	B96695	hypothetical prote	363	69.5	5.8	1704	2	A59188	ATP-binding casset
291	70	5.9	189	2	T51847	manganese-binding	364	69.5	5.8	1778	2	JT0382	apolipoprotein B -
292	70	5.9	199	2	T08902	protein F113.8 [im	365	69.5	5.8	2629	2	I46569	apolipoprotein B -
293	70	5.9	213	2	F86310	hypothetical prote	366	69.5	5.8	7829	2	T15789	hypothetical prote
294	70	5.9	256	2	T13597	hypothetical prote	367	69	5.8	169	2	E83941	hypothetical prote
295	70	5.9	287	2	T52317	chlorophyll a/b-bi	368	69	5.8	195	2	A96998	CDP-diglyceride sy
296	70	5.9	292	2	H64244	H+-transporting tw	369	69	5.8	244	2	H96934	uncharacterized me
297	70	5.9	307	2	E95010	ABC transporter, p	370	69	5.8	256	2	C64145	hypothetical prote
298	70	5.9	307	2	B97882	hypothetical prote	371	69	5.8	261	2	T07481	hypothetical prote
299	70	5.9	330	2	T30981	hypothetical prote	372	69	5.8	273	2	F83805	hypothetical prote
300	70	5.9	333	2	I38974	G protein-coupled	373	69	5.8	273	2	C71707	hypothetical prote
301	70	5.9	371	2	T46421	hypothetical prote	374	69	5.8	289	2	S72554	melatonin receptor
302	70	5.9	388	2	A55597	oxytocin receptor	375	69	5.8	291	2	D96002	probable sugar upt
303	70	5.9	416	2	A85112	probable ankyrin-r	376	69	5.8	300	2	T32702	hypothetical prote
304	70	5.9	418	2	T08982	proline/betaine tr	377	69	5.8	308	2	A99979	hypothetical prote
305	70	5.9	420	2	E72357	sugar ABC transpor	378	69	5.8	339	2	B69436	LSU ribosomal prot
306	70	5.9	427	2	T01905	hypothetical prote	379	69	5.8	345	2	AH1514	hypothetical prote
307	70	5.9	437	2	C91261	glutamate-aspartat	380	69	5.8	351	2	AD0273	probable integral
308	70	5.9	437	2	G86101	glutamate-aspartat	381	69	5.8	379	2	S58447	ubiquinol-cytochro
309	70	5.9	438	2	AF3215	ABC transporter, m	382	69	5.8	382	2	A13175	conserved hypothet
310	70	5.9	450	2	T42595	envelope protein 5	383	69	5.8	383	2	D71424	hypothetical prote
311	70	5.9	494	2	B89827	hypothetical prote	384	69	5.8	388	2	I69644	O-antigen polymera
312	70	5.9	532	2	T49467	related to COPI-in	385	69	5.8	436	2	T11268	NADH2 dehydrogenas
313	70	5.9	551	2	A87019	probable cytochrom	386	69	5.8	437	2	A42384	glutamate-aspartat
314	70	5.9	554	2	T27878	hypothetical prote	387	69	5.8	443	2	T19512	hypothetical prote
315	70	5.9	558	2	H72565	hypothetical prote	388	69	5.8	478	2	S25821	transposase - Baci
316	70	5.9	675	2	T22323	hypothetical prote	389	69	5.8	478	2	T33985	probable thioredox
317	70	5.9	735	2	S46830	urea transport pro	390	69	5.8	508	2	E96804	hypothetical prote
318	70	5.9	963	2	T26022	hypothetical prote	391	69	5.8	523	2	T11916	NADH2 dehydrogenas
319	70	5.9	1930	2	F86200	protein F12K11.17	392	69	5.8	540	2	T24675	hypothetical prote
320	69.5	5.8	133	1	MNIHHC	nonstructural prot	393	69	5.8	549	2	E70784	cytochrome b homol
321	69.5	5.8	206	2	S76279	hypothetical prote	394	69	5.8	579	2	A64100	inner membrane cop

395	69	5.8	599	2	G90476	probable Na+/H+ an	468	68	5.7	426	2	C69831	conserved hypothet
396	69	5.8	600	2	T11889	NADH2 dehydrogenas	469	68	5.7	464	2	C70414	NADH2 dehydrogenas
397	69	5.8	637	2	H96592	probable multispan	470	68	5.7	473	2	H71044	cytochomel-proce
398	69	5.8	659	2	D84633	probable multispan	471	68	5.7	475	2	B83450	cytochrome-c oxida
399	69	5.8	791	2	T12455	hypothetical prote	472	68	5.7	477	2	H91123	probable oxidoredu
400	69	5.8	802	2	JH0595	potassium channel	473	68	5.7	477	2	G85968	probable oxidoredu
401	69	5.8	863	2	H84490	hypothetical prote	474	68	5.7	477	2	C65096	hypothetical 52.1
402	69	5.8	933	2	AD3309	hypothetical membr	475	68	5.7	488	2	A53572	prostaglandin E2 r
403	69	5.8	1058	2	T30580	P-type ATPase - sl	476	68	5.7	502	1	I30010	NADH2 dehydrogenas
404	69	5.8	1344	2	T34188	myb-binding protei	477	68	5.7	519	2	T39918	probable acetyl-co
405	69	5.8	1392	2	T01908	hypothetical prote	478	68	5.7	542	2	A69261	probable acid-CoA
406	69	5.8	1515	2	T04204	hypothetical prote	479	68	5.7	542	2	B81910	probable ABC-trans
407	69	5.8	3010	1	A45573	genome polyprotein	480	68	5.7	542	2	E81105	ABC transporter A
408	68.5	5.7	225	2	AE0371	probable carboxype	481	68	5.7	620	2	T19907	hypothetical prote
409	68.5	5.7	237	2	T25877	hypothetical prote	482	68	5.7	664	2	C84869	probable receptor
410	68.5	5.7	238	2	T04280	hypothetical prote	483	68	5.7	718	2	E83718	hypothetical prote
411	68.5	5.7	260	2	H75428	hypothetical prote	484	68	5.7	804	2	T49975	hypothetical prote
412	68.5	5.7	262	2	AG1830	hypothetical prote	485	68	5.7	836	2	T18460	hypothetical prote
413	68.5	5.7	265	2	A13428	O-antigen export s	486	68	5.7	859	2	S69700	hypothetical prote
414	68.5	5.7	285	2	E68835	maltose ABC transp	487	68	5.7	871	2	H72597	hypothetical prote
415	68.5	5.7	297	2	S74335	carbon dioxide con	488	68	5.7	1429	2	T19422	hypothetical prote
416	68.5	5.7	304	2	AG3035	hypothetical prote	489	68	5.7	1878	2	E86189	hypothetical prote
417	68.5	5.7	304	2	D98250	probable sugar ABC	490	68	5.7	3010	1	GNWVTC	genome polyprotein
418	68.5	5.7	343	2	AC3129	iron(III) dicitrat	491	67.5	5.6	104	2	T36801	hypothetical prote
419	68.5	5.7	359	2	B55105	hypothetical prote	492	67.5	5.6	200	2	H72295	conserved hypothet
420	68.5	5.7	362	2	D72424	oligopeptide ABC t	493	67.5	5.6	273	2	A97700	hypothetical prote
421	68.5	5.7	377	1	JQ2337	omega-3 fatty acid	494	67.5	5.6	288	2	F72219	conserved hypothet
422	68.5	5.7	383	2	I53870	Edg-1 orphan recep	495	67.5	5.6	320	2	T23674	hypothetical prote
423	68.5	5.7	391	2	H81265	probable transmemb	496	67.5	5.6	323	1	QOBE03	HHRF3 protein - hu
424	68.5	5.7	395	2	B83774	hypothetical prote	497	67.5	5.6	348	2	T12591	NADH2 dehydrogenas
425	68.5	5.7	395	2	A96189	hypothetical prote	498	67.5	5.6	354	2	T09353	G protein-coupled
426	68.5	5.7	395	2	AH3097	conserved hypothet	499	67.5	5.6	362	2	C88086	protein TILP1.1 (i
427	68.5	5.7	419	2	AG1660	multidrug resistan	500	67.5	5.6	387	2	T24581	hypothetical prote
428	68.5	5.7	420	2	I51666	Mel-1c receptor su	501	67.5	5.6	397	2	A83999	mutants block spor
429	68.5	5.7	425	2	F97108	probable glycosyl	502	67.5	5.6	419	2	AH1288	multidrug resistan
430	68.5	5.7	430	2	S15308	hypothetical prote	503	67.5	5.6	439	2	H83699	sodium-dependent c
431	68.5	5.7	431	2	H72247	preprotein translo	504	67.5	5.6	450	2	G91219	TDP-Fuc4NAc lipid
432	68.5	5.7	444	2	A48260	corticosterin trans	505	67.5	5.6	450	2	A86066	TDP-Fuc4NAc lipid
433	68.5	5.7	445	2	E22845	hypothetical prote	506	67.5	5.6	450	2	F65183	4-alpha-l-fucosyl
434	68.5	5.7	479	2	T44326	hypothetical prote	507	67.5	5.6	452	2	G89870	hypothetical prote
435	68.5	5.7	480	2	B70446	hypothetical prote	508	67.5	5.6	459	2	JH0594	vasoactive intesti
436	68.5	5.7	488	2	T15941	hypothetical prote	509	67.5	5.6	483	2	G84113	hypothetical prote
437	68.5	5.7	492	2	G90574	hypothetical prote	510	67.5	5.6	488	1	QXASM4	NADH2 dehydrogenas
438	68.5	5.7	502	2	T07731	NADH2 dehydrogenas	511	67.5	5.6	492	2	F64464	sodium-dependent n
439	68.5	5.7	512	2	T00605	probable cytochrom	512	67.5	5.6	498	2	T48262	hypothetical prote
440	68.5	5.7	518	2	S50465	PAC2 protein - ya	513	67.5	5.6	516	2	E72089	ADP, ATP carrier p
441	68.5	5.7	525	2	JN0902	pituitary adenylat	514	67.5	5.6	516	2	H82973	choline transport
442	68.5	5.7	542	2	S59102	hypothetical prote	515	67.5	5.6	598	2	I51368	gamma-aminobutyric
443	68.5	5.7	558	2	F64235	Na+ ATPase chain J	516	67.5	5.6	632	2	A71259	probable dicarboxy
444	68.5	5.7	634	2	C83530	potassium uptake p	517	67.5	5.6	676	1	WZVZ18	I8 protein - vacci
445	68.5	5.7	670	2	G86702	potassium uptake p	518	67.5	5.6	676	2	T37345	I8 protein - vacci
446	68.5	5.7	724	2	H86427	unknown protein (i	519	67.5	5.6	676	2	D42511	I8 protein - vacci
447	68.5	5.7	788	2	G64707	cation-transportin	520	67.5	5.6	676	2	F36843	ATP/GRP-binding pr
448	68.5	5.7	923	1	MMBY7C	probable membrane	521	67.5	5.6	676	2	T28500	hypothetical prote
449	68.5	5.7	1004	1	S55353	probable copper-tr	522	67.5	5.6	682	2	D72158	L8R protein - vari
450	68	5.7	146	2	H75201	hypothetical prote	523	67.5	5.6	686	2	G82448	sensor histidine k
451	68	5.7	205	2	A64373	hypothetical prote	524	67.5	5.6	716	2	S30687	hypothetical prote
452	68	5.7	255	2	F39925	hypothetical prote	525	67.5	5.6	740	1	T02567	probable ATP-bindi
453	68	5.7	266	2	C95316	probable ABC trans	526	67.5	5.6	838	2	A54163	vacuolar ATPase (B
454	68	5.7	270	2	AE3627	maltose transport	527	67.5	5.6	866	2	T20574	hypothetical prote
455	68	5.7	279	2	AG2165	bicarbonate transp	528	67.5	5.6	950	2	T15915	hypothetical prote
456	68	5.7	294	2	T41953	G protein-coupled	529	67.5	5.6	1159	2	T02866	hypothetical prote
457	68	5.7	294	2	AE0004	ribonuclease BN (B	530	67.5	5.6	1244	2	T19615	hypothetical prote
458	68	5.7	313	2	B38888	COI intron 9 prote	531	67.5	5.6	1411	2	S48442	PDR1 protein - ye
459	68	5.7	355	2	A45177	chemokine (C-C) re	532	67.5	5.6	1753	2	S30855	hypothetical prote
460	68	5.7	360	2	T11067	ubiquinol-cytochro	533	67.5	5.6	2332	1	GNYP	genome polyprotein
461	68	5.7	364	2	JC2115	prostaglandin E re	534	67	5.6	151	2	A72093	conserved hypothet
462	68	5.7	365	2	JN0693	prostaglandin E2 r	535	67	5.6	151	2	H86529	CT101 hypothet
463	68	5.7	370	2	H90559	hypothetical prote	536	67	5.6	159	2	S61040	probable membrane
464	68	5.7	379	2	S58450	ubiquinol-cytochro	537	67	5.6	180	2	I48129	Xel69 (escapes x-1
465	68	5.7	393	2	AG0184	probable multidrug	538	67	5.6	203	2	D70150	hypothetical prote
466	68	5.7	402	2	T41253	hypothetical wtf5	539	67	5.6	225	1	MMIIB	E1 membrane glycop
467	68	5.7	417	2	T11387	NADH2 dehydrogenas	540	67	5.6	244	2	D70404	conserved hypothet

541	67	5.6	255	2	C90078	hypothetical prote	614	66.5	5.6	412	2	G89773	hypothetical prote
542	67	5.6	275	2	G98194	sugar ABC transpor	615	66.5	5.6	413	2	H95041	polysaccharide tra
543	67	5.6	275	2	AC3092	hypothetical prote	616	66.5	5.6	435	2	D98111	hypothetical prote
544	67	5.6	275	2	S75698	hypothetical prote	617	66.5	5.6	435	2	G95246	maltodextrin ABC t
545	67	5.6	276	2	F69307	conserved hypothet	618	66.5	5.6	453	2	B95135	MATE efflux family
546	67	5.6	276	2	S35270	DNA-damage repair	619	66.5	5.6	462	2	H71228	hypothetical prote
547	67	5.6	283	2	F96959	tRNA-processing ri	620	66.5	5.6	488	2	G71969	cytochrome-c oxida
548	67	5.6	285	2	AE3024	hypothetical prote	621	66.5	5.6	490	2	D84998	low-affinity inorg
549	67	5.6	286	2	D64235	hypothetical prote	622	66.5	5.6	490	2	D84998	CAMP receptor subt
550	67	5.6	314	2	D96703	hypothetical prote	623	66.5	5.6	491	2	AC6391	efflux transporter
551	67	5.6	317	2	D98260	inner membrane pro	624	66.5	5.6	493	2	AC1555	hypothetical prote
552	67	5.6	336	2	A96997	ferrichrome transp	625	66.5	5.6	494	2	A71875	hypothetical prote
553	67	5.6	345	2	T21776	hypothetical prote	626	66.5	5.6	507	2	T27627	hypothetical prote
554	67	5.6	349	2	D84166	hypothetical prote	627	66.5	5.6	539	2	G83720	nickel transport s
555	67	5.6	350	2	C88987	protein C50H11.2 [628	66.5	5.6	547	2	E91135	probable alkaline
556	67	5.6	352	2	T32314	hypothetical prote	629	66.5	5.6	547	2	H85980	probable alkaline
557	67	5.6	379	2	S58451	ubiquinol-cytochro	630	66.5	5.6	550	1	A48026	sterol O-acyltrans
558	67	5.6	379	2	S58449	ubiquinol-cytochro	631	66.5	5.6	582	2	C71424	hypothetical prote
559	67	5.6	396	1	C69291	pheromone shutdown	632	66.5	5.6	583	2	A11510	C-terminal domain
560	67	5.6	407	2	E70309	hypothetical prote	633	66.5	5.6	598	2	T32430	hypothetical prote
561	67	5.6	411	2	B71500	probable amino aci	634	66.5	5.6	663	2	AG2696	cytochrome c-type
562	67	5.6	415	2	S74041	pyruvate synthase	635	66.5	5.6	663	2	G97478	cytochrome c-type
563	67	5.6	416	2	T46401	hypothetical prote	636	66.5	5.6	727	2	IS6506	Na+/Cl(-)-depend
564	67	5.6	423	2	C95085	sodium-dependent t	637	66.5	5.6	727	2	S27043	neurotransmitter t
565	67	5.6	436	2	AC1021	proton glutamate s	638	66.5	5.6	782	2	S19876	genome polyprotein
566	67	5.6	441	2	F86279	hypothetical prote	639	66.5	5.6	862	2	B36786	hypothetical prote
567	67	5.6	446	2	G72287	hypothetical prote	640	66.5	5.6	889	2	T47311	hypothetical prote
568	67	5.6	496	2	A31986	glucose transporte	641	66.5	5.6	992	2	T27479	hypothetical prote
569	67	5.6	507	2	AB1707	glycine betaine tr	642	66.5	5.6	1014	2	T31433	Na+/Ca2+,K+-exchan
570	67	5.6	516	2	AE0665	probable membrane	643	66.5	5.6	1083	2	C88854	protein Flia10.3 [
571	67	5.6	646	2	JC7777	ATP binding casset	644	66.5	5.6	1144	2	H81037	DNA polymerase III
572	67	5.6	717	2	T49238	hypothetical prote	645	66.5	5.6	1456	2	T15961	hypothetical prote
573	67	5.6	753	2	S58331	dolichyl-phosphate	646	66.5	5.6	1584	2	JW0057	gravin - human
574	67	5.6	769	2	F81415	DNA topoisomerase	647	66.5	5.6	1768	2	E85062	hypothetical prote
575	67	5.6	784	2	C82679	cell division prot	648	66.5	5.6	2151	1	S16449	genome polyprotein
576	67	5.6	787	2	PN0677	hypothetical prote	649	66.5	5.6	2285	1	G02434	DNA-directed DNA p
577	67	5.6	798	2	T34248	hypothetical prote	650	66.5	5.6	2833	2	A43360	inositol 1,4,5-tri
578	67	5.6	814	2	T05537	probable serine/th	651	66.5	5.6	3011	1	GNWVC3	genome polyprotein
579	67	5.6	823	2	T35280	probable integral	652	66.5	5.6	93	2	S28759	NADH2 dehydrogenas
580	67	5.6	880	2	D69427	conserved hypothet	653	66.5	5.6	130	2	D83820	diacylglycerol kin
581	67	5.6	891	2	B82495	probable NADH dehy	654	66.5	5.6	209	2	A89801	conserved hypothet
582	67	5.6	900	2	E69631	galactosamine-cont	655	66.5	5.6	276	2	H96816	hypothetical prote
583	67	5.6	1175	2	S39951	chitin synthase (E	656	66.5	5.6	279	2	S42125	hypothetical prote
584	67	5.6	1242	1	DJBEC1	DNA-directed DNA p	657	66.5	5.6	285	2	D87447	sulfate ABC transp
585	67	5.6	1333	2	S63403	probable membrane	658	66.5	5.6	302	2	A99074	hypothetical prote
586	67	5.6	1511	2	A53151	pleiotropic drug r	659	66.5	5.6	305	2	I47040	sterol O-acyltrans
587	67	5.6	1575	2	G82905	conserved hypothet	660	66.5	5.6	317	1	B41671	iron transport pro
588	67	5.6	1879	2	T19481	hypothetical prote	661	66.5	5.6	318	2	B84291	hypothetical prote
589	67	5.6	1905	2	T18267	multidrug resistan	662	66.5	5.6	322	2	E71137	hypothetical prote
590	67	5.6	1993	2	T30902	sodium channel SCA	663	66.5	5.6	332	2	C97272	conserved membrane
591	67	5.6	3010	1	GNWVCJ	genome polyprotein	664	66.5	5.6	370	1	IS2315	G protein-coupled
592	66.5	5.6	153	1	G69847	conserved hypothet	665	66.5	5.6	379	1	S17405	ubiquinol-cytochro
593	66.5	5.6	203	2	T28732	hypothetical prote	666	66.5	5.6	379	1	S17409	ubiquinol-cytochro
594	66.5	5.6	204	2	C70506	hypothetical prote	667	66.5	5.6	379	2	S58460	G protein-coupled
595	66.5	5.6	218	2	C64586	cag pathogenicity	668	66.5	5.6	381	2	A35300	protein UL33 - hum
596	66.5	5.6	245	2	A81405	sec-independent pr	669	66.5	5.6	390	1	QOBET9	hypothetical prote
597	66.5	5.6	263	2	A12384	hypothetical prote	670	66.5	5.6	397	2	T21154	hypothetical prote
598	66.5	5.6	268	2	A70417	hypothetical prote	671	66.5	5.6	397	2	T44477	hypothetical prote
599	66.5	5.6	272	2	AI0075	probable permease	672	66.5	5.6	397	2	B70505	probable emulsan r
600	66.5	5.6	279	1	S56642	nitrate transport	673	66.5	5.6	401	2	T44831	probable sugar tra
601	66.5	5.6	279	2	E70322	hypothetical prote	674	66.5	5.6	404	2	B64927	probable transport
602	66.5	5.6	293	2	A84110	sugar ABC transpor	675	66.5	5.6	404	2	A85777	probable transport
603	66.5	5.6	294	2	S70876	hypothetical prote	676	66.5	5.6	404	2	E90928	CBS domain protein
604	66.5	5.6	316	2	F81712	ABC transporter, p	677	66.5	5.6	411	2	H86539	GGDEF family prote
605	66.5	5.6	333	2	S77103	hypothetical prote	678	66.5	5.6	412	2	A82444	hypothetical wtfs
606	66.5	5.6	347	2	AD2201	hypothetical prote	679	66.5	5.6	418	2	T41027	hypothetical prote
607	66.5	5.6	356	2	T20737	hypothetical prote	680	66.5	5.6	424	2	B72353	probable phosphati
608	66.5	5.6	359	2	F90055	conserved hypothet	681	66.5	5.6	428	2	T07366	hypothetical prote
609	66.5	5.6	367	2	S75836	hypothetical prote	682	66.5	5.6	436	2	T14816	hypothetical prote
610	66.5	5.6	380	2	G89786	hypothetical prote	683	66.5	5.6	447	2	T18633	alpha-2B-adrenergi
611	66.5	5.6	384	1	I38890	dual specificity p	684	66.5	5.6	450	2	A37223	alpha-2-adrenergi
612	66.5	5.6	389	2	E96516	Fl6N3.13 [imported	685	66.5	5.6	450	2	A38316	ABC transporter pe
613	66.5	5.6	400	2	G00013	D3 dopamine recept	686	66.5	5.6	453	2	F86846	

687	66	5.5	483	2	S75369	hypothenical prote	760	65.5	5.5	561	2	S71189	Dwarfl protein - A
688	66	5.5	484	2	T24238	hypothenical prote	761	65.5	5.5	575	2	AH1417	ABC transporter (A
689	66	5.5	496	2	E82940	hypothenical prote	762	65.5	5.5	578	2	TI5736	hypothenical prote
690	66	5.5	508	2	G47677	hypothenical prote	763	65.5	5.5	583	2	AH1151	glycerophosphoryl
691	66	5.5	525	2	T28306	PTS MSV145 hypothe	764	65.5	5.5	590	2	C81316	probable sugar epi
692	66	5.5	527	2	G69635	RTS arbutin-like e	765	65.5	5.5	597	2	B82881	hypothenical prote
693	66	5.5	532	2	A90037	hypothenical prote	766	65.5	5.5	617	2	AB1167	phosphotransferase
694	66	5.5	536	2	A69890	hypothenical prote	767	65.5	5.5	618	2	AC1204	phosphotransferase
695	66	5.5	548	2	B87423	cytochrome-c oxida	768	65.5	5.5	642	2	H70331	ATP-dependent heli
696	66	5.5	552	2	S45886	hypothenical prote	769	65.5	5.5	718	2	A56851	Na+/myo-inositol c
697	66	5.5	565	2	S73707	Na(+) translocatin	770	65.5	5.5	720	2	H82198	Rtx toxin transpor
698	66	5.5	570	2	S07744	NADH2 dehydrogenas	771	65.5	5.5	721	2	AF1254	penicillin-binding
699	66	5.5	573	1	S33212	INDA1 protein - fu	772	65.5	5.5	740	2	S61568	probable membrane
700	66	5.5	573	2	AF1418	ABC transporter, A	773	65.5	5.5	860	1	QRHULD	LDL receptor precu
701	66	5.5	573	2	AH1793	ABC transporter, A	774	65.5	5.5	858	2	AC0204	probable integral
702	66	5.5	619	2	TI1314	NADH2 dehydrogenas	775	65.5	5.5	1087	1	S41797	cellulose 1,4-beta
703	66	5.5	632	2	T24405	hypothenical prote	776	65.5	5.5	1328	2	B22999	tyB protein - yea
704	66	5.5	654	2	A98350	hypothenical ABC t	777	65.5	5.5	1427	2	S74293	SRB8 protein - yea
705	66	5.5	654	2	AF2932	hypothenical prote	778	65.5	5.5	1581	2	B71636	hypothenical prote
706	66	5.5	705	2	T48464	hypothenical prote	779	65.5	5.5	1635	2	T32452	hypothenical prote
707	66	5.5	721	2	A70764	probable glgK prot	780	65	5.4	126	2	AD0340	probable membrane
708	66	5.5	736	2	G01522	acidic 82 kDa prot	781	65	5.4	149	2	C69393	transcription regu
709	66	5.5	784	2	B90442	tricorn proteinase	782	65	5.4	176	1	QIAD25	early E1B 21K prot
710	66	5.5	1039	2	S76747	hypothenical prote	783	65	5.4	196	2	S40728	hypothenical prote
711	66	5.5	1054	2	A61221	probable calcium t	784	65	5.4	225	1	MMIHIV	E1 membrane glycop
712	66	5.5	1359	2	T34036	hypothenical prote	785	65	5.4	247	2	I48149	serotonin receptor
713	66	5.5	1375	2	S48375	hypothenical prote	786	65	5.4	257	2	B75099	hypothenical prote
714	66	5.5	2599	2	F90608	ABC transporter pe	787	65	5.4	259	2	A47112	growth response pr
715	66	5.5	26926	1	I38344	titin, cardiac mus	788	65	5.4	271	2	E89950	hema concentration
716	65.5	5.5	132	2	E97760	NADH2 dehydrogenas	789	65	5.4	280	2	S75957	nitrate transport
717	65.5	5.5	132	2	E70074	hypothenical prote	790	65	5.4	290	2	T02877	probable chlorophy
718	65.5	5.5	146	2	G69447	hypothenical prote	791	65	5.4	291	2	C97453	cytochrome c oxida
719	65.5	5.5	171	2	A13476	signal peptidase I	792	65	5.4	291	2	AB2671	cytochrome c oxida
720	65.5	5.5	197	2	T17106	hypothenical prote	793	65	5.4	307	2	B36125	branched-chain ami
721	65.5	5.5	210	2	S67771	endoplasmic reticu	794	65	5.4	313	2	A64084	lysophospholipase
722	65.5	5.5	252	2	T43100	hypothenical prote	795	65	5.4	322	2	D87087	hypothenical prote
723	65.5	5.5	290	2	F68456	signal sequence pe	796	65	5.4	322	2	S38091	hypothenical prote
724	65.5	5.5	297	2	F86839	phosphate ABC tran	797	65	5.4	330	2	H75068	dipeptide abc tran
725	65.5	5.5	297	2	E83792	hypothenical prote	798	65	5.4	335	2	H75029	hypothenical prote
726	65.5	5.5	301	2	T21308	hypothenical prote	799	65	5.4	338	2	S50339	NADH2 dehydrogenas
727	65.5	5.5	317	2	S23459	polysulfide reduct	800	65	5.4	344	2	AD1200	conserved hypothe
728	65.5	5.5	327	2	T36087	probable binding p	801	65	5.4	345	2	T12361	NADH2 dehydrogenas
729	65.5	5.5	348	1	S36003	NADH2 dehydrogenas	802	65	5.4	355	2	G70200	hypothenical prote
730	65.5	5.5	351	2	F82880	hypothenical ferri	803	65	5.4	359	2	T15249	hypothenical prote
731	65.5	5.5	365	1	F69629	spore germination	804	65	5.4	362	2	H69785	mannan endo-1,4-be
732	65.5	5.5	367	2	JC2056	ubiquinol-cytochro	805	65	5.4	375	2	I38879	corticotropin rele
733	65.5	5.5	379	2	S58456	ubiquinol-cytochro	806	65	5.4	379	1	S17414	ubiquinol-cytochro
734	65.5	5.5	379	2	T32778	hypothenical prote	807	65	5.4	379	2	S58461	ubiquinol-cytochro
735	65.5	5.5	391	2	T32601	hypothenical prote	808	65	5.4	379	2	S58455	ubiquinol-cytochro
736	65.5	5.5	394	2	AH0362	nucleoside permeas	809	65	5.4	380	1	D34285	ubiquinol-cytochro
737	65.5	5.5	410	2	T11064	NADH2 dehydrogenas	810	65	5.4	382	2	T11138	ubiquinol-cytochro
738	65.5	5.5	423	2	E90569	conserved hypothe	811	65	5.4	390	2	C84984	hypothenical prote
739	65.5	5.5	425	2	A97688	hypothenical 45.5K	812	65	5.4	415	2	T21532	hypothenical prote
740	65.5	5.5	425	2	AF2913	conserved hypothe	813	65	5.4	438	2	B81410	probable integral
741	65.5	5.5	429	2	T32832	hypothenical prote	814	65	5.4	442	2	A83122	probable MFS trans
742	65.5	5.5	442	2	A42670	microfibril-associ	815	65	5.4	445	2	AD2358	glucosyltransferas
743	65.5	5.5	445	2	T38916	probable transcrip	816	65	5.4	457	2	T28334	Ser/Thr protein ki
744	65.5	5.5	449	2	H83629	probable dicarboxy	817	65	5.4	462	2	B88613	protein T27B9.5 [1
745	65.5	5.5	457	2	A75327	hypothenical prote	818	65	5.4	477	2	S54508	probable membrane
746	65.5	5.5	477	2	B75170	hypothenical prote	819	65	5.4	479	2	A69036	TRK system potassi
747	65.5	5.5	480	2	A60043	endoplasmic reticu	820	65	5.4	481	2	E81050	cytochrome-c oxida
748	65.5	5.5	487	2	A97928	type I site-specif	821	65	5.4	490	2	T14545	probable sugar tra
749	65.5	5.5	488	1	H64537	cytochrome-c oxida	822	65	5.4	492	2	S59107	NADH2 dehydrogenas
750	65.5	5.5	488	2	G81295	cytochrome-c oxida	823	65	5.4	510	2	S55204	hypothenical prote
751	65.5	5.5	491	2	AB1197	efflux transporter	824	65	5.4	511	2	H75097	polysaccharide bio
752	65.5	5.5	495	2	A97022	probably membrane	825	65	5.4	513	2	T37180	probable membrane
753	65.5	5.5	500	2	G84706	hypothenical prote	826	65	5.4	526	2	D91047	hydrogenase 4 memb
754	65.5	5.5	502	2	AD3395	NADH2 dehydrogenas	827	65	5.4	530	2	B89771	hypothenical prote
755	65.5	5.5	502	2	T25669	hypothenical prote	828	65	5.4	535	2	A64697	conserved hypothe
756	65.5	5.5	518	2	A53207	probable folate tr	829	65	5.4	539	2	S55190	hypothenical prote
757	65.5	5.5	528	2	T34417	delayed rectifier	830	65	5.4	547	2	T31543	hypothenical prote
758	65.5	5.5	544	2	B84825	probable ABC trans	831	65	5.4	547	2	S53920	SN1 protein - yea
759	65.5	5.5	545	2	E90460	hypothenical prote	832	65	5.4	576	2	T25375	hypothenical prote

833	65	5.4	579	2	S61131	probable membrane	906	64.5	5.4	495	2	S36114	pituitary adenylat
834	65	5.4	608	2	S65298	dicarboxylic amino	907	64.5	5.4	495	2	S10851	glycinin G1 precu
835	65	5.4	611	2	T21747	hypothetical prote	908	64.5	5.4	512	2	H64964	probable membrane
836	65	5.4	624	2	G82508	hypothetical prote	909	64.5	5.4	521	2	A99549	amino acid permea
837	65	5.4	627	2	T11125	NADH2 dehydrogenas	910	64.5	5.4	523	2	S39060	pituitary adenylat
838	65	5.4	633	2	F84483	Mutator-like trans	911	64.5	5.4	547	2	H65107	hypothetical 61.6
839	65	5.4	638	2	D69957	conserved hypothet	912	64.5	5.4	554	2	A56730	carl protein - Pod
840	65	5.4	643	2	F97787	sodium/pantothenat	913	64.5	5.4	555	2	B97812	virulence factor m
841	65	5.4	676	2	A45515	dnak-type molecula	914	64.5	5.4	575	2	AB1793	ABC transporter (A
842	65	5.4	684	2	F86394	protein T2P13.20	915	64.5	5.4	576	2	T05904	cytochrome P450 97
843	65	5.4	687	2	H84791	hypothetical prote	916	64.5	5.4	614	2	B89869	hypothetical prote
844	65	5.4	702	2	T13505	NADH2 dehydrogenas	917	64.5	5.4	622	2	AC1236	acyltransferase (c
845	65	5.4	705	2	T04400	NADH2 dehydrogenas	918	64.5	5.4	638	1	Q0BY2M	mRNA maturase b14
846	65	5.4	773	2	H96918	hypothetical prote	919	64.5	5.4	715	2	T26307	hypothetical prote
847	65	5.4	773	2	G83816	late competence op	920	64.5	5.4	720	2	T47648	ABC transporter-li
848	65	5.4	808	2	T04459	hypothetical prote	921	64.5	5.4	721	2	AD1617	penicillin-binding
849	65	5.4	861	2	S77086	hypothetical prote	922	64.5	5.4	721	2	AE1491	hypothetical prote
850	65	5.4	927	2	T38518	ribonuclease II RN	923	64.5	5.4	735	2	AD0341	probable membrane
851	65	5.4	931	2	F84637	probable plasma me	924	64.5	5.4	763	2	AD1070	phosphatidylglycer
852	65	5.4	938	2	T01809	hypothetical prote	925	64.5	5.4	801	2	A89862	Na+/H+ antiporter
853	65	5.4	1089	2	C70522	probable mmp18 pro	926	64.5	5.4	803	2	H64568	histidine kinase -
854	65	5.4	1163	2	D64315	type I restriction	927	64.5	5.4	889	2	T30715	probable major cor
855	65	5.4	1178	2	S76370	sensory transducti	928	64.5	5.4	979	2	A70848	probable membrane
856	65	5.4	1232	2	T38496	anion exchanger 3	929	64.5	5.4	1007	2	JC8066	138K protein - Tet
857	65	5.4	1421	2	T34225	hypothetical prote	930	64.5	5.4	1114	2	JH0284	125K surface antig
858	65	5.4	5069	2	T17464	rifamycin polyketi	931	64.5	5.4	1146	2	B70723	probable mmp112 pr
859	64.5	5.4	180	2	T41339	hypothetical prote	932	64.5	5.4	1154	2	T48829	related to SREBP c
860	64.5	5.4	211	2	S35280	eac protein - phag	933	64.5	5.4	1465	2	S45628	DNA-directed DNA p
861	64.5	5.4	217	2	AE0395	probable amino aci	934	64.5	5.4	1529	2	S69688	hypothetical prote
862	64.5	5.4	227	2	C69432	hypothetical prote	935	64.5	5.4	1630	2	S64403	ESPI protein - yea
863	64.5	5.4	234	2	F69657	HAD superfamily hy	936	64.5	5.4	1661	2	S64800	probable membrane
864	64.5	5.4	268	2	AF2470	potassium channel	937	64.5	5.4	3033	1	GNWVJ8	genome polypeptid
865	64.5	5.4	271	2	B81384	prolipoprotein dia	938	64	5.4	202	2	A70041	conserved hypothet
866	64.5	5.4	275	2	T43119	hypothetical prote	939	64	5.4	209	2	G82359	cdd3 protein - Clo
867	64.5	5.4	283	2	D71517	probable metal tra	940	64	5.4	253	2	JC5347	hypothetical prote
868	64.5	5.4	295	2	T22202	hypothetical prote	941	64	5.4	259	2	T12451	conserved hypothet
869	64.5	5.4	297	2	T27584	hypothetical prote	942	64	5.4	269	2	H69768	protein F13E6.3 [i
870	64.5	5.4	320	2	T23904	hypothetical prote	943	64	5.4	270	2	F89632	probable ABC-type
871	64.5	5.4	326	2	A86411	protein F3W18.6 [i	944	64	5.4	274	2	T50567	plant-metabolite d
872	64.5	5.4	333	2	F64175	hypothetical prote	945	64	5.4	276	2	C70040	probable membrane
873	64.5	5.4	358	2	T22823	hypothetical prote	946	64	5.4	276	2	S48358	probable sugar upt
874	64.5	5.4	361	2	A86841	hypothetical prote	947	64	5.4	281	2	C95932	probable permease
875	64.5	5.4	361	2	A40734	Pas (Passover) pro	948	64	5.4	283	2	B83009	sugar transport sy
876	64.5	5.4	379	1	S43264	ubiquinol-cytochro	949	64	5.4	285	2	B83883	cytochrome-c oxida
877	64.5	5.4	379	2	T11505	ubiquinol-cytochro	950	64	5.4	288	2	S36955	hypothetical prote
878	64.5	5.4	379	2	S58454	ubiquinol-cytochro	951	64	5.4	330	2	T28675	dopamine receptor
879	64.5	5.4	379	2	A53077	ubiquinol-cytochro	952	64	5.4	342	2	A48258	NADH2 dehydrogenas
880	64.5	5.4	381	1	CBMS	ubiquinol-cytochro	953	64	5.4	347	2	T11248	protein kinase SPK
881	64.5	5.4	381	2	S33449	pituitary adenylat	954	64	5.4	351	2	S56716	PL6 protein - huma
882	64.5	5.4	385	2	H69154	hypothetical prote	955	64	5.4	351	2	G01430	hypothetical prote
883	64.5	5.4	388	2	H95057	phosphoglycerate k	956	64	5.4	367	2	T20271	hypothetical prote
884	64.5	5.4	398	2	A97927	phosphoglycerate k	957	64	5.4	369	2	H90587	ubiquinol-cytochro
885	64.5	5.4	400	2	G01977	d3 dopamine recept	958	64	5.4	370	1	S26031	twitching motility
886	64.5	5.4	411	2	S46800	LAGI protein - yea	959	64	5.4	376	2	G82656	probable cytochrom
887	64.5	5.4	416	2	AF1127	rod shape-determin	960	64	5.4	378	2	D64181	ubiquinol-cytochro
888	64.5	5.4	426	2	T45800	UDP-N-acetylglucos	961	64	5.4	379	1	CBBO	ubiquinol-cytochro
889	64.5	5.4	433	2	T11162	NADH2 dehydrogenas	962	64	5.4	379	1	S17419	ubiquinol-cytochro
890	64.5	5.4	435	2	AC0105	probable maltodext	963	64	5.4	379	1	S26163	ubiquinol-cytochro
891	64.5	5.4	439	2	C22845	NADH2 dehydrogenas	964	64	5.4	379	1	S43263	ubiquinol-cytochro
892	64.5	5.4	439	2	A84153	hypothetical prote	965	64	5.4	379	2	T11414	ubiquinol-cytochro
893	64.5	5.4	443	2	B26696	hypothetical prote	966	64	5.4	379	2	S58452	ubiquinol-cytochro
894	64.5	5.4	444	2	T11474	NADH2 dehydrogenas	967	64	5.4	379	2	S58459	ubiquinol-cytochro
895	64.5	5.4	444	2	A43676	P44 hepatitis-asso	968	64	5.4	383	2	S55594	G protein-coupled
896	64.5	5.4	444	2	S48218	microtubular aggre	969	64	5.4	383	2	G64667	NA+/H+ antiporter
897	64.5	5.4	446	1	DYRTD3	dopamine receptor	970	64	5.4	383	2	H71848	probable na+/h+ an
898	64.5	5.4	448	2	D85362	hypothetical prote	971	64	5.4	387	2	S74522	hypothetical prote
899	64.5	5.4	448	2	S57909	probable histidine	972	64	5.4	402	2	AD1417	drug-efflux transp
900	64.5	5.4	450	2	T23288	hypothetical prote	973	64	5.4	404	2	A97559	hypothetical prote
901	64.5	5.4	451	2	D70045	two-component sens	974	64	5.4	404	2	AE2779	acyltransferase [i
902	64.5	5.4	467	2	JN0616	pituitary adenylat	975	64	5.4	409	2	S26021	NADH2 dehydrogenas
903	64.5	5.4	478	2	C29051	transposase C - Ba	976	64	5.4	411	2	A55610	corticotropin-rele
904	64.5	5.4	495	1	FWSYG2	glycinin chain Ala	977	64	5.4	413	2	H81659	branched-chain ami
905	64.5	5.4	495	2	S39061	pituitary adenylat	978	64	5.4	422	2	E84338	isocitrate dehydro

979	64	5.4	430	1	S32570	malc protein - Str	1052	63.5	5.3	327	2	S56162	MDCR15 protein - h
980	64	5.4	450	2	B40392	alpha-2-adrenergic	1053	63.5	5.3	328	2	D38215	oligopeptide ABC t
981	64	5.4	451	2	A36908	spore cortex penic	1054	63.5	5.3	328	2	T39824	septin homolog - f
982	64	5.4	455	2	T31258	aromatic oxygenase	1055	63.5	5.3	334	2	B72393	oligopeptide ABC t
983	64	5.4	457	2	AF2975	aminotransferase,	1056	63.5	5.3	334	2	T41037	hypothetical prote
984	64	5.4	457	2	E98307	probable aminotran	1057	63.5	5.3	334	2	T27081	hypothetical prote
985	64	5.4	463	2	AC0281	probable amino aci	1058	63.5	5.3	342	2	A38908	spa40 protein - Sh
986	64	5.4	469	2	H90322	polysaccharide bio	1059	63.5	5.3	344	2	T34981	probable integral
987	64	5.4	492	2	E58931	NADH2 dehydrogenas	1060	63.5	5.3	355	2	T15203	hypothetical prote
988	64	5.4	503	2	JC7627	cytochrome P450 3A	1061	63.5	5.3	359	2	D90172	hypothetical prote
989	64	5.4	511	2	T40334	hypothetical prote	1062	63.5	5.3	361	2	AE3071	hypothetical prote
990	64	5.4	527	2	A75122	sodium- and chlori	1063	63.5	5.3	365	2	AB3494	oligopeptide trans
991	64	5.4	536	2	T38109	hypothetical prote	1064	63.5	5.3	372	2	S26667	G protein-coupled
992	64	5.4	538	2	C90406	conserved hypothet	1065	63.5	5.3	377	2	B72275	probable aspartate
993	64	5.4	544	2	T13877	NADH2 dehydrogenas	1066	63.5	5.3	380	1	CBRT	ubiquinol-cytochro
994	64	5.4	562	2	T52481	cytochrome-c oxida	1067	63.5	5.3	381	2	T11312	ubiquinol-cytochro
995	64	5.4	575	2	G75282	probable glutathio	1068	63.5	5.3	387	2	H88012	protein K10B4.2 (i
996	64	5.4	586	1	A34400	ezrin [validated]	1069	63.5	5.3	389	2	G75133	hypothetical prote
997	64	5.4	598	2	T05130	hypothetical prote	1070	63.5	5.3	392	2	H71520	probable hth trans
998	64	5.4	602	2	C75120	hypothetical prote	1071	63.5	5.3	395	2	B81358	transmembrane tran
999	64	5.4	606	2	B69805	conserved hypothet	1072	63.5	5.3	398	2	C71682	ubiquinol-cytochro
1000	64	5.4	608	2	G02640	polycyclic kidney	1073	63.5	5.3	398	2	D81397	probable periplasm
1001	64	5.4	609	2	F70512	probable ATPase -	1074	63.5	5.3	399	2	B95080	cell division prot
1002	64	5.4	610	2	S37049	H+-exporting ATPas	1075	63.5	5.3	400	2	AG3016	phosphoglycerate k
1003	64	5.4	614	2	A69845	Na+/H+ antiporter	1076	63.5	5.3	401	2	T46306	hypothetical prote
1004	64	5.4	630	2	T47177	hypothetical prote	1077	63.5	5.3	404	1	LABECA	latent membrane pr
1005	64	5.4	654	2	C86677	DNA ligase (NAD) (1078	63.5	5.3	406	2	T19887	hypothetical prote
1006	64	5.4	657	2	T52460	hypothetical prote	1079	63.5	5.3	423	2	T04915	CDP-diacylglycerol
1007	64	5.4	661	2	T51779	non-phototropic hy	1080	63.5	5.3	423	2	G85255	CDP-diacylglycerol
1008	64	5.4	674	2	T50347	hypothetical prote	1081	63.5	5.3	426	2	A96268	phosphoglycerate k
1009	64	5.4	696	2	AB1566	hypothetical prote	1082	63.5	5.3	426	2	T33299	hypothetical prote
1010	64	5.4	748	2	T10651	hypothetical prote	1083	63.5	5.3	438	2	A82262	conserved hypothet
1011	64	5.4	802	2	AB7754	protein C43E11.11	1084	63.5	5.3	444	2	B85789	hypothetical prote
1012	64	5.4	838	2	H82939	conserved hypothet	1085	63.5	5.3	445	2	T16025	hypothetical prote
1013	64	5.4	860	2	T37768	probable vacuolar	1086	63.5	5.3	447	2	F90940	hypothetical prote
1014	64	5.4	874	2	B86322	F6A14.8 protein -	1087	63.5	5.3	447	2	S52437	CDP-diacylglycerol
1015	64	5.4	896	2	AF1409	the two components	1088	63.5	5.3	450	2	E96738	hypothetical prote
1016	64	5.4	991	2	S57385	probable membrane	1089	63.5	5.3	452	2	T21118	sugar transferase
1017	64	5.4	1024	1	RN2QBF	DNA-directed RNA p	1090	63.5	5.3	461	2	C97187	hypothetical prote
1018	64	5.4	1078	2	T19745	hypothetical prote	1091	63.5	5.3	468	2	T48686	mg2+ transport pro
1019	64	5.4	1081	2	B81303	probable membrane	1092	63.5	5.3	485	2	H90562	hypothetical prote
1020	64	5.4	1227	2	A31638	erythrocyte anion	1093	63.5	5.3	487	2	B95059	hypothetical prote
1021	64	5.4	1385	2	T13415	hypothetical prote	1094	63.5	5.3	491	2	A64939	hypothetical prote
1022	64	5.4	1462	1	DJHUAC	DNA-directed DNA p	1095	63.5	5.3	492	2	B50373	sugar transport re
1023	64	5.4	1695	2	JE0084	voltage-gated sodi	1096	63.5	5.3	494	2	S76516	integral membrane
1024	64	5.4	2496	2	A71616	secreted protein P	1097	63.5	5.3	498	2	T48385	transporter like p
1025	63.5	5.3	111	2	S43115	acidic ribosomal p	1098	63.5	5.3	498	2	T16190	NADH dehydrogenase
1026	63.5	5.3	123	2	G71692	NADH2 dehydrogenas	1099	63.5	5.3	500	2	AF2325	hypothetical prote
1027	63.5	5.3	147	2	AH0495	probable membrane	1100	63.5	5.3	511	2	G90321	virulence factor m
1028	63.5	5.3	149	2	H70581	hypothetical prote	1101	63.5	5.3	512	1	A70201	conserved hypothet
1029	63.5	5.3	195	2	E71000	hypothetical prote	1102	63.5	5.3	525	2	A49601	nucleoscapid prote
1030	63.5	5.3	214	2	C90191	conserved hypothet	1103	63.5	5.3	537	2	G82873	sterol O-acyltrans
1031	63.5	5.3	218	2	B71925	cag island protein	1104	63.5	5.3	540	1	I49454	uncharacterized me
1032	63.5	5.3	218	2	T29205	hypothetical prote	1105	63.5	5.3	544	2	C96943	l-lactate permease
1033	63.5	5.3	231	2	F85679	probable antirepre	1106	63.5	5.3	551	2	E64537	l-lactate permease
1034	63.5	5.3	238	2	S75336	hypothetical prote	1107	63.5	5.3	551	2	D71969	probable peptide t
1035	63.5	5.3	241	2	F86691	ABC transporter pe	1108	63.5	5.3	555	2	G96744	probable l-lactate
1036	63.5	5.3	242	1	S74794	hypothetical prote	1109	63.5	5.3	567	2	C75340	hyaluronoglucosam
1037	63.5	5.3	246	2	AD3574	branched-chain ami	1110	63.5	5.3	568	2	T17588	sodium/dicarboxyla
1038	63.5	5.3	259	2	AF0106	probable membrane	1111	63.5	5.3	593	2	I46528	protein ZK697.5 (i
1039	63.5	5.3	275	2	E95161	hypothetical prote	1112	63.5	5.3	594	2	E88956	glucose transport
1040	63.5	5.3	275	2	D98027	hypothetical prote	1113	63.5	5.3	605	2	A36361	probable flagellar
1041	63.5	5.3	275	2	G84320	hypothetical prote	1114	63.5	5.3	605	2	H71562	hypothetical prote
1042	63.5	5.3	276	2	E96951	conserved membrane	1115	63.5	5.3	605	2	T43974	hypothetical prote
1043	63.5	5.3	280	2	T16240	hypothetical prote	1116	63.5	5.3	610	2	T44161	hypothetical prote
1044	63.5	5.3	282	2	B83086	conserved hypothet	1117	63.5	5.3	668	2	B54759	ba-type ubiquinol
1045	63.5	5.3	282	2	AB0346	probable ABC trans	1118	63.5	5.3	671	2	B37237	protein kinase C (
1046	63.5	5.3	291	2	AB2939	hypothetical prote	1119	63.5	5.3	681	2	AF0697	probable type III
1047	63.5	5.3	291	2	E98343	hypothetical prote	1120	63.5	5.3	683	2	A85044	hypothetical prote
1048	63.5	5.3	291	2	F75571	hypothetical prote	1121	63.5	5.3	708	2	JQ1148	killer toxin KHS p
1049	63.5	5.3	313	2	D26696	NADH2 dehydrogenas	1122	63.5	5.3	741	2	T20314	hypothetical prote
1050	63.5	5.3	315	2	E69365	hypothetical prote	1123	63.5	5.3	780	2	T48189	probable transport
1051	63.5	5.3	316	2	H86665	ferrichrome ABC tr	1124	63.5	5.3	787	2	A70132	cell division prot

1125	63.5	5.3	819	2	T19351	hypothetical prote	1198	63	5.3	480	2	B70367	hypothetical prote
1126	63.5	5.3	841	2	T38703	hypothetical prote	1199	63	5.3	481	2	S60260	stomatin-like prot
1127	63.5	5.3	843	2	T32487	hypothetical prote	1200	63	5.3	490	2	C71541	probable na-depend
1128	63.5	5.3	843	2	T41237	conserved hypochet	1201	63	5.3	491	2	AC1499	transmembrane prot
1129	63.5	5.3	844	2	AD2339	hypothetical prote	1202	63	5.3	493	2	T02376	hypothetical prote
1130	63.5	5.3	951	2	T08987	probable cadmium-t	1203	63	5.3	494	2	T14246	NADH2 dehydrogenas
1131	63.5	5.3	966	2	H97717	hypothetical prote	1204	63	5.3	508	2	E90594	amino acid permeas
1132	63.5	5.3	1004	2	G87323	hypothetical prote	1205	63	5.3	509	1	A48528	membrane glycoprot
1133	63.5	5.3	1098	2	S38100	hypothetical prote	1206	63	5.3	527	2	T40744	probable nuclear d
1134	63.5	5.3	1229	2	S42391	SIP3 protein - yea	1207	63	5.3	531	2	AH1491	hypothetical prote
1135	63.5	5.3	1351	2	C71607	hypothetical prote	1208	63	5.3	533	2	T06153	hypothetical prote
1136	63.5	5.3	1388	2	T17269	hypothetical prote	1209	63	5.3	534	2	A99316	hypothetical prote
1137	63.5	5.3	1407	1	T00558	probable ABC trans	1210	63	5.3	535	2	AF1835	hypothetical prote
1138	63.5	5.3	1408	2	T47671	P-glycoprotein-lik	1211	63	5.3	562	2	B70081	hypothetical prote
1139	63.5	5.3	1545	2	T42751	sulfonylurea recep	1212	63	5.3	565	2	B86359	protein Similar to
1140	63.5	5.3	1545	2	T46645	sulfonylurea recep	1213	63	5.3	569	2	C70136	flagellar basal-bo
1141	63.5	5.3	1769	2	S53378	probable membrane	1214	63	5.3	574	2	T47566	hypothetical prote
1142	63.5	5.3	2357	2	A59249	class VII unconven	1215	63	5.3	579	2	AB2177	hypothetical prote
1143	63.5	5.3	4725	1	A44357	dynein heavy chain	1216	63	5.3	583	2	G84829	probable PRK2 fami
1144	63	5.3	96	1	WMV2P3	F3 protein - fowlp	1217	63	5.3	594	2	G89789	two-component sens
1145	63	5.3	103	2	T20878	hypothetical prote	1218	63	5.3	598	2	S66954	probable membrane
1146	63	5.3	175	2	D70945	hypothetical prote	1219	63	5.3	600	2	B83875	two-component sens
1147	63	5.3	230	2	B81705	conserved hypochet	1220	63	5.3	608	2	AD2000	ABC transporter AT
1148	63	5.3	230	2	T17506	hypothetical prote	1221	63	5.3	677	2	T26574	hypothetical prote
1149	63	5.3	236	2	F83520	phosphoribosylamin	1222	63	5.3	677	2	F95910	replication licens
1150	63	5.3	249	2	T01891	hypothetical prote	1223	63	5.3	682	1	H64485	NADH2 dehydrogenas
1151	63	5.3	257	2	S01165	achaete-scute locu	1224	63	5.3	701	2	T13568	NADH2 dehydrogenas
1152	63	5.3	258	2	H65188	sec-independent pr	1225	63	5.3	702	2	T12677	NADH2 dehydrogenas
1153	63	5.3	258	2	F86071	sec-independent pr	1226	63	5.3	704	2	T13665	NADH2 dehydrogenas
1154	63	5.3	258	2	H91224	Sec-independent pr	1227	63	5.3	712	2	D87418	proton pump, proba
1155	63	5.3	280	2	D84015	maltose/maltodextr	1228	63	5.3	729	2	T06127	probable sugar tra
1156	63	5.3	288	2	S36954	cytochrome-c oxida	1229	63	5.3	737	2	I39547	S-protein secretio
1157	63	5.3	290	2	S48301	geranylgeranyl tra	1230	63	5.3	738	2	S58612	NADH2 dehydrogenas
1158	63	5.3	301	2	T50001	hypothetical prote	1231	63	5.3	769	2	G95270	hypothetical prote
1159	63	5.3	306	2	H83620	probable permease	1232	63	5.3	813	2	T02672	hypothetical prote
1160	63	5.3	313	2	A86743	hypothetical prote	1233	63	5.3	849	2	C87740	protein H26D21.2 l
1161	63	5.3	322	2	B90013	hypothetical prote	1234	63	5.3	869	2	S49844	probable membrane
1162	63	5.3	329	2	B87790	protein B0207.4 [i	1235	63	5.3	943	2	B45082	neutrotrophic recep
1163	63	5.3	332	2	B84943	hypothetical prote	1236	63	5.3	960	2	T17297	hypothetical prote
1164	63	5.3	339	2	D89880	conserved hypochet	1237	63	5.3	1030	2	A42497	anion exchanger 3,
1165	63	5.3	345	2	T12364	NADH2 dehydrogenas	1238	63	5.3	1034	2	B86880	SWI/SNF family hel
1166	63	5.3	358	2	B83808	hypothetical prote	1239	63	5.3	1082	2	H70360	cation efflux syst
1167	63	5.3	359	2	S56720	probable serine/th	1240	63	5.3	1212	2	B82809	exodeoxyribonuclea
1168	63	5.3	361	2	A45211	prostaglandin E re	1241	63	5.3	1227	2	B34911	band 3-related pro
1169	63	5.3	362	2	C69804	surface adhesion h	1242	63	5.3	1532	2	T18438	hypothetical prote
1170	63	5.3	362	2	T29552	hypothetical prote	1243	63	5.3	1646	2	JH0422	voltage-dependent
1171	63	5.3	364	2	S65009	prostaglandin E re	1244	63	5.3	1854	2	T39035	putative sodium ch
1172	63	5.3	365	2	A42414	prostaglandin E re	1245	63	5.3	2203	2	T42742	voltage-dependent
1173	63	5.3	378	1	S17412	ubiquinol-cytochro	1246	63	5.3	2295	2	B71621	probable membrane
1174	63	5.3	379	1	S17411	ubiquinol-cytochro	1247	63	5.3	4488	1	RR1HM2	genome polypeptin
1175	63	5.3	379	1	S41833	ubiquinol-cytochro	1248	62.5	5.2	107	2	B69262	hypothetical prote
1176	63	5.3	379	1	S41847	ubiquinol-cytochro	1249	62.5	5.2	140	2	B86739	potassium channel
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1178	63	5.3	379	2	T11492	ubiquinol-cytochro	1251	62.5	5.2	168	2	JC1169	DNA-damage-inducib
1179	63	5.3	379	2	S58085	ubiquinol-cytochro	1252	62.5	5.2	173	2	D71702	hypothetical prote
1180	63	5.3	379	2	S58464	ubiquinol-cytochro	1253	62.5	5.2	178	2	S67379	hypothetical prote
1181	63	5.3	382	2	S47882	ubiquinol-cytochro	1254	62.5	5.2	181	2	G82911	hypothetical prote
1182	63	5.3	386	2	S60646	NADH2 dehydrogenas	1255	62.5	5.2	200	2	A71895	hypothetical prote
1183	63	5.3	389	2	H95003	aromatic amino aci	1256	62.5	5.2	232	2	T22698	hypothetical prote
1184	63	5.3	389	2	C97876	aspartate transami	1257	62.5	5.2	236	2	F83705	hypothetical prote
1185	63	5.3	391	2	D64541	molybdopterin bios	1258	62.5	5.2	240	2	H70091	hypothetical prote
1186	63	5.3	396	2	E97947	cell division prot	1259	62.5	5.2	244	2	T20810	hypothetical prote
1187	63	5.3	398	2	B70415	proton/sodium-glut	1260	62.5	5.2	245	2	S10658	hypothetical prote
1188	63	5.3	405	2	T29002	hypothetical prote	1261	62.5	5.2	258	2	E91201	type III secretion
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1191	63	5.3	420	2	A57742	cyclin Ia - maize	1264	62.5	5.2	274	2	G72292	sorbitol/mannitol
1192	63	5.3	431	2	T23809	hypothetical prote	1265	62.5	5.2	276	2	H83568	probable permease
1193	63	5.3	448	2	T30982	hypothetical prote	1266	62.5	5.2	276	2	H83568	hypothetical prote
1194	63	5.3	450	2	A34169	alpha-2A-adrenergi	1267	62.5	5.2	280	2	T24579	NADH2 dehydrogenas
1195	63	5.3	469	2	AE2188	hypothetical prote	1268	62.5	5.2	283	2	T11063	NADH2 dehydrogenas
1196	63	5.3	475	2	S52893	hypothetical prote	1269	62.5	5.2	289	2	D82504	phosphate ABC tran
1197	63	5.3	478	2	C59095	hypothetical prote	1270	62.5	5.2	293	2	AH0075	probable permease

1271	62.5	5.2	296	2	H83480	cytochrome o ubiqu	1344	62.5	5.2	704	2	S46000	probable membrane
1272	62.5	5.2	298	2	T37251	homeobox protein c	1345	62.5	5.2	718	2	T05840	subtilisin-like pr
1273	62.5	5.2	299	2	T26365	hypothetical prote	1346	62.5	5.2	763	2	T27937	hypothetical prote
1274	62.5	5.2	326	2	C90272	hypothetical prote	1347	62.5	5.2	807	2	T28279	ORF MSV19 probabl
1275	62.5	5.2	333	2	AB1925	hypothetical prote	1348	62.5	5.2	815	2	G97266	mannose-1-phosphat
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1277	62.5	5.2	335	2	T41426	hypothetical wtf8	1350	62.5	5.2	848	2	A33810	band 3 anion trans
1278	62.5	5.2	349	2	H95060	ABC transporter, p	1351	62.5	5.2	865	2	AB1658	probable membrane
1279	62.5	5.2	349	2	D97929	hypothetical prote	1352	62.5	5.2	881	2	G96574	hypothetical prote
1280	62.5	5.2	352	2	E81450	probable integral	1353	62.5	5.2	971	2	H71719	hypothetical prote
1281	62.5	5.2	358	2	E83829	hypothetical prote	1354	62.5	5.2	1082	2	T41988	hypothetical prote
1282	62.5	5.2	365	2	F82210	amino acid ABC tra	1355	62.5	5.2	1144	2	A81983	probable DNA-dirc
1283	62.5	5.2	369	2	C88030	protein F46F5.10 [1356	62.5	5.2	1195	2	C87691	hypothetical prote
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1286	62.5	5.2	379	2	S58462	ubiquinol-cytochro	1359	62.5	5.2	1397	2	E87998	hypothetical prote
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1288	62.5	5.2	382	2	A72373	conserved hypotet	1361	62.5	5.2	1676	2	E71410	probable centromer
1289	62.5	5.2	383	1	A44227	omega-3 fatty acid	1362	62.5	5.2	1687	2	T43144	vitellogenin II pr
1290	62.5	5.2	383	2	F84771	hypothetical prote	1363	62.5	5.2	1951	2	B43963	hypothetical prote
1291	62.5	5.2	383	2	T31738	hypothetical prote	1364	62.5	5.2	2150	2	S13553	NADH2 dehydrogenas
1292	62.5	5.2	388	2	C64722	Na+/H+-exchanging	1365	62	5.2	112	2	T11073	hypothetical prote
1293	62.5	5.2	391	2	A86632	aromatic amino aci	1366	62	5.2	132	2	D82954	cell-shape determi
1294	62.5	5.2	399	2	H84087	hypothetical prote	1367	62	5.2	174	2	E84028	colicin B immunity
1295	62.5	5.2	404	2	H83249	sodium/glutamate s	1368	62	5.2	175	1	IMECB	uncharacterized co
1296	62.5	5.2	405	1	QQBE35	BBRF3 protein - hu	1369	62	5.2	198	2	E97217	hypothetical prote
1297	62.5	5.2	409	2	H89006	protein T22F3.11 [1370	62	5.2	201	2	G90134	conserved hypotet
1298	62.5	5.2	409	2	C89942	conserved hypotet	1371	62	5.2	206	2	F99840	protein F37C4.1 [i
1299	62.5	5.2	413	2	AC1169	multidrug resistanc	1372	62	5.2	209	2	A88656	hypothetical prote
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1301	62.5	5.2	420	2	D95018	conserved hypotet	1374	62	5.2	225	2	B65127	probable phosphoea
1302	62.5	5.2	420	2	E97891	conserved hypotet	1375	62	5.2	242	1	F75433	potassium channel
1303	62.5	5.2	422	2	C70518	probable nant prot	1376	62	5.2	247	2	AC1332	dihydrolipoamide S
1304	62.5	5.2	425	2	E97172	flagellin [importe	1377	62	5.2	273	2	E70010	probable sugar upt
1305	62.5	5.2	426	2	A72080	ct266 hypothetical	1378	62	5.2	285	2	H95943	transcription regu
1306	62.5	5.2	426	2	E86542	CT266 hypothetical	1379	62	5.2	287	2	A69838	cytochrome-c oxida
1307	62.5	5.2	431	2	H84069	hypothetical prote	1380	62	5.2	288	2	S36953	probable permease
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1312	62.5	5.2	452	2	G64844	probable membrane	1385	62	5.2	312	2	S48851	chalcone reductase
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1315	62.5	5.2	455	2	D97217	UDP-N-acetylmuramo	1388	62	5.2	331	2	AB3117	hypothetical prote
1316	62.5	5.2	457	2	F69662	high-affinity bran	1389	62	5.2	334	2	T05987	hypothetical prote
1317	62.5	5.2	459	2	AF3284	probable mannosyl	1390	62	5.2	345	2	T32203	hypothetical prote
1318	62.5	5.2	461	2	S57713	inositol 1,4,5-tri	1391	62	5.2	351	2	C86408	F3H9.12 protein -
1319	62.5	5.2	468	2	A91331	hypothetical prote	1392	62	5.2	352	2	C98170	hypothetical prote
1320	62.5	5.2	470	2	C70641	hypothetical prote	1393	62	5.2	353	2	T42971	hypothetical prote
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1322	62.5	5.2	490	2	T40116	hypothetical prote	1395	62	5.2	360	2	T33260	hypothetical prote
1323	62.5	5.2	492	2	AC0768	probable transmemb	1396	62	5.2	362	2	B57641	G protein-coupled
1324	62.5	5.2	494	2	T15502	hypothetical prote	1397	62	5.2	363	2	S42379	hypothetical prote
1325	62.5	5.2	501	1	JN0539	head protein gp5 -	1398	62	5.2	370	2	H84111	response regulator
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1331	62.5	5.2	568	2	S64567	hypothetical prote	1404	62	5.2	398	1	E64112	hypothetical prote
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1335	62.5	5.2	580	2	T02596	NADH2 dehydrogenas	1409	62	5.2	402	2	D70186	conserved hypotet
1336	62.5	5.2	601	2	T11451	hypothetical prote	1410	62	5.2	403	2	B69338	cbs domain protein
1337	62.5	5.2	608	2	T34391	myosin-light-chain	1411	62	5.2	411	2	H72084	protein-tyrosine-p
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1417 62 5.2 458 2 A84487 probable replicati
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1490 61.5 5.1 278 2 D83080 hypothetical prote
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1493 61.5 5.1 289 2 F91269 hypothetical prote
1494 61.5 5.1 289 2 D86110 hypothetical prote
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1496 61.5 5.1 292 2 AE1539 sugar ABC transport
1497 61.5 5.1 293 2 C90032 hypothetical prote
1498 61.5 5.1 293 2 A83710 ABC transporter (p
1499 61.5 5.1 293 2 B69866 transcritpion regu
1500 61.5 5.1 294 2 AD0886 probable oxidoredu

ALIGNMENTS

RESULT 1
I38027
MLN 64 protein - human
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: I38027; S60682
R:Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lidereau, R.
Genomics 28, 367-376, 1995
A:Title: Identification of four novel human genes amplified and overexpressed in breast
A:Reference number: I37080; MUID:96039245; PMID:7490069
A:Accession: I38027
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-445 <RES>
A:Cross-references: UNIPROT:Q14849; UNIPARC:UPI000012F1BC; EMBL:X80198; NID:g951278; PI
A:Note: submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Gene: MLN64

Query Match 55.6%; Score 664; DB 2; Length 445;
Best Local Similarity 56.2%; Pred. No. 8.7e-55;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;
QY 1 MHLP-----EDMENAL-----TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
DB 1 MSKLPRLTRDLERSLPVAVASLGSSLSQSLSHLLPPPE-----KRRASIDV 49
QY 52 RTEFCLFVTFDILLFVTLWIIELNVNGGIENTLEKVMQDYVSSYFDIFLLAVPRFKVL 111
DB 50 RTEFCLFVTFDILLFVTLWIIELNTGIRKNLEQEIIOINFKTSFFDIFVLAFPRFSG 109
QY 112 ILAYAVCLRHRHWAIALTAVTSAFLAKVILSKLFSQAGFYVLPILISFILAWIETWFL 171
DB 110 LLGYAVQLRHHWVIAVTLVSSAFLVKVILSELLSKAGFYVLPILISFILAWIETWFL 169
QY 172 DFKVLPQEAEEENRLLIVODASERAAI--PGGLSDGQFYSPPESEAGSB-EAEKKQDSK 229
DB 170 DFKVLPQEAEEERWVLAQVAVARGPFLFSGALSEQFYSPPESEAGSDNESDEAVGKK 229

RESULT 2
Tl6170
hypothetical protein F26F4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Tl6170
R:Pulton, L.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of C. elegans cosmid F26F4.
A:Reference number: Z18471
A:Accession: Tl6170
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-478 <FUL>
A:Cross-references: UNIPROT:Q19819; UNIPARC:UPI000017B938; EMBL:U12964; NID:g1213452; P
A:Experimental source: strain Bristol N2
C:Genetics:


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Qy   157 PIISFLAMTETWLFDFKULPQ-EASEENRLLIIVQDASERAALI 199
      ||| | | | | | | | | | | | | | | | | | | | | |
Db   334 PYLEFVACNIE--FKGRILANLEGGKEGSSAIINLNKAALM 375

RESULT 8
A$7219
Batten disease-related protein CLN3 - human
C$Species: Homo sapiens (man)
C$Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C$Accession: A57219
R:Lerner, T.J.; Boustany, R.M.N.; Anderson, J.W.; D'Arigo, K.L.; Schlumpf, K.; Buckler, E.M.; de Vos, N.; van Ommen, G.J.B.; Breuning, M.H.; Doggett, N.A.; Meincke, L.J.; Liu, C.; Mole, S.E.
Cell 82, 949-957, 1995
A>Title: Isolation of a novel gene underlying Batten disease, CLN3.
A$Reference number: A57219; MUID:96016090; PMID:7553855
A$Accession: A57219
A>Status: preliminary; not compared with conceptual translation
A$Molecule type: mRNA
A$Residues: 1-438 <LER>
A$Cross-references: UNIPROT:Q13286; UNIPARC:UPI00000000ED; GB:U32680; NID:g1039422; PID:
C$Genetics:
A$Gene: GDB:CLN3
A$Cross-references: GDB:120593; OMIM:204200
A$Map position: 16p12.1-16p11.2
C$Superfamily: CLN3 protein/Battenin (Batten disease protein)
C$Keywords: membrane protein

Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 3.4;
Matches 38; Conservative 18; Mismatches 46; Indels 47; Gaps 8;

Ov    64 LFVTLLWII-----ELNVNGGI-----ENTILEKEVMQYDYISSYFDIELLAVFRF 108

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009
QY 109 KVLILAYAVCRLRHWMAIALTTVAITSFAFLKLVLSQGAGFVLIIPSL----- 163
 | | | | | | | | | | | | | | |
Db 334 R---SSLRCCRIRFTWALALLQCINLNVFLADV-----WFGF-LPSIYLVLFIILY 380

QY 164 -----AWLETWFLDPKVLPOEAEENR 185
 | | | | | | | | | | | | | | |
Db 381 EGLGGAAVYNT----FHNIALETSDEHR 405

RESULT 9
G70172
conserved hypothetical integral membrane protein BB0584 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: G70172
R:Fraser, C.M.; Castjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whitson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, B.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: G70172
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-448 <XLE>
A:Cross-references: UNIPROT:O51531; UNIPARC:UPI0000005752F; GB:AE001160; GB:AE000783; NT:
A:Experimental source: strain B31

Query Match 7.1%; Score 85; DB 2; Length 448;
Best Local Similarity 24.4%; Pred. No. 3.9;
Matches 47; Conservative 28; Mismatches 64; Indels 54; Gaps 11;

QY 50 DVARTTCLFVTPLDLFVTL-----LWIELNANGIE-NTLEKEVMQDYISS-----Y 97
 | | | | | | | | | | | | | | |

A;Gene: ND5
 A;Genome: mitochondrion
 A;Genetic code: SGC6
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.9%; Score 83; DB 1; Length 590;
 Best Local Similarity 23.9%; Pred. No. 8.3;
 Matches 32; Conservative 23; Mismatches 37; Indels 42; Gaps 7;
 QY 55 FCLFVTF-----DLL---FVTLWIELNVNGIENTLEKEVMQDYSSYDFIFLLAVF 106
 Db 95 FILFYAFYMYDMLKRFENIFWVFLCNFFI-----LSYDLYTAYCGWELGLF 146
 QY 107 RFKVLILAYAVCLRHHWAIATVATSAFLAKVILSKLFSQAGYVLPPIISFILAWI 166
 Db 147 SF--FLISY-----FWRFALKFGKSFISKI-----GDVILLUSFWNTFI 187
 QY 167 ET-----WFLDF 173
 Db 188 STCYGMINFYVNF 201

RESULT 14
 B29835
 Tras protein - Escherichia coli plasmid pED208
 C;Species: Escherichia coli
 C;Date: 04-Aug-1988 #sequence_revision 04-Aug-1988 #text_change 09-Jul-2004
 C;Accession: B29835
 R;Finlay, B.B.; Paranchych, W.
 J. Bacteriol. 166, 713-721, 1986
 A;Title: Nucleotide sequence of the surface exclusion genes tras and trat from the IncP-4
 A;Reference number: A29835; MUID:86223783; PMID:3011738
 A;Accession: B29835
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-186 <PIN>
 A;Cross-references: UNIPROT:P14498; UNIPARC:UPI0000001563
 C;Genetics:
 A;Genome: plasmid

Query Match 6.9%; Score 82.5; DB 2; Length 186;
 Best Local Similarity 23.8%; Pred. No. 2.4;
 Matches 31; Conservative 24; Mismatches 40; Indels 35; Gaps 6;
 QY 61 FDLFVTLWIELNVNGIENTLEKEVMQDYSSYDFIFLL-----AVFREKVLILAY 115
 Db 44 FQLLFI----IFDIFINSNR-----DYH--YFDTFVITLGSNAFFSLVFLMSTY 87
 QY 116 AVCRLRHHWAIATVATSAFLAKVILSKLFSQAGYVLPPII-----SFLAW 165
 Db 88 NLVSLK-----ISLGSEITEQSVLLKVERKINSYGQPLMVVNAIVGCVLLSSGERFVAGL 143
 QY 166 IETWFLDFKV 175
 Db 144 GFSWFVYLI 153

RESULT 15
 C64227
 hypothetical protein homolog MG247 - Mycoplasma genitalium
 C;Species: Mycoplasma genitalium
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: C64227
 R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
 M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
 C.A.; Venter, J.C
 Science 270, 397-403, 1995
 A;Title: The minimal gene complement of Mycoplasma genitalium.
 A;Reference number: A64200; MUID:96026346; PMID:7569993
 A;Accession: C64227
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA

A;Residues: 1-239 <TIGR>
 A;Cross-references: UNIPROT:P47489; UNIPARC:UPI00001394F7; GB:U39703; GB:L43967; NID:931
 A;Experimental source: strain G-37
 C;Genetics:
 A;Genetic code: SGC3
 C;Superfamily: Escherichia coli ygiH protein

Query Match 6.9%; Score 82.5; DB 1; Length 239;
 Best Local Similarity 21.7%; Pred. No. 3.2;
 Matches 33; Conservative 26; Mismatches 54; Indels 39; Gaps 8;
 QY 42 GREKKGISDVRRTF-----CLFVTFDILLFVTL--WIELNVNGIENTLEKEVMQYD 92
 Db 42 GSKNPGATNSMRVGLKIGLVAIFDAFKGFFAFLLTWIL---FRFGLOGYLTKVYQST 98
 QY 93 YYSSEYDFILLAV-----FRK-----VLLILAYAVCLRHHWAI-----ALTTAVTSA 135
 Db 99 YFLSYLSGCAATIGHTIFPYFKPGKKAJATGGSLLAISLWFLICLLIWIWITLITKY 158
 QY 136 FLIAKVLISKLFSQAGYVLPPIISFILAWIE 167
 Db 159 VSLASLITF-----FVLAVI-ILIPALD 180

Search completed: December 30, 2006, 16:49:57
 Job time : 68 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 30, 2006, 16:49:17 ; Search time 300 seconds
(without alignments)
721.512 Million cell updates/sec

Title: US-10-063-519-14

Perfect score: 1195

Sequence: 1 MNHLPEMDENALTGSSSHA.....EAGSEAEKQDSEKPLLEL 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score Greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	234	1	MENTO_HUMAN
2	1141.5	95.5	235	2	Q5U205_RAT
3	1134.5	94.9	235	1	MENTO_MOUSE
4	1134.5	94.9	235	2	Q3U8Q7_MOUSE
5	1128.5	94.4	235	2	Q3U852_MOUSE
6	796	66.6	227	2	Q6DI38_BRARE
7	700.5	58.6	448	2	Q6DFR7_XENTR
8	698.5	58.5	444	2	Q6PFA0_XENLA
9	684	57.2	448	2	Q6GNT3_XENLA
10	664	55.6	445	1	MLN64_HUMAN
11	664	55.6	445	2	Q3Y533_HUMAN
12	656.5	54.9	446	1	MLN64_MOUSE
13	656.5	54.9	446	2	Q544C3_MOUSE
14	656.5	54.9	446	2	Q5U2T5_RAT
15	632	52.9	448	1	MLN64_BRARE
16	586.5	49.1	444	2	Q4S943_TETNG
17	566	47.4	501	2	Q5RB70_PONPY
18	364.5	30.5	574	2	Q563D1_AEDAE
19	364.5	30.5	595	2	Q563D0_AEDAE
20	346	29.0	523	2	Q7QIT3_ANOGA
21	343	28.7	545	2	Q6MZ44_DROME
22	343	28.7	583	2	Q9W145_DROSOPHILA
23	342.5	28.7	131	2	Q4THH5_TETNG
24	330	27.6	476	2	Q3V5Y6_BOMMO
25	272	22.8	197	2	Q4SNJ2_TETNG
26	209.5	17.5	185	2	Q5BVU9_SCHJA
27	206.5	17.3	419	2	Q6OZ70_CAEBR
28	204	17.1	447	2	Q19819_CAEBEL
29	181.5	15.2	141	2	Q4SNJ3_TETNG
30	117	9.8	459	2	Q46F23_METBA
31	104.5	8.7	294	1	MLN64_SALFO
					Q90Zb9 salvelinus
					Q95772 homo sapien
					Q5u205 rattus norv
					Q3dc13 mus musculu
					Q3u8q7 mus musculu
					Q3u852 mus musculu
					Q6di38 brachydanio
					Q6df7 xenopus tro
					Q6pf40 xenopus lae
					Q5gnt3 xenopus lae
					Q14849 homo sapien
					Q53y53 homo sapien
					Q61542 mus musculu
					Q544c3 m 3 days ne
					Q5u2t5 rattus norv
					Q3dfsa brachydanio
					Q4s943 tetraodon n
					Q5rb70 pongo pygma
					Q563d1 aedes aegyp
					Q563d0 aedes aegyp
					Q7qit3 anopheles g
					Q6mzh4 drosophila
					Q9w145 drosophila
					Q3v5y6 bombyx mori
					Q4snj2 tetraodon n
					Q5bv9 schistosoma
					Q6oz70 caenorhabdi
					Q19819 caenorhabdi
					Q4snj3 tetraodon n
					Q46f23 methanosaec
					Q90zb9 salvelinus

Q97YQ0 SULSO	2	348	8.6	102.5	32
Q31et4 sulfolobus	2	369	8.4	100.5	33
Q31et4 theileria p	2	348	8.4	100.5	34
Q4n7c1 theileria p	2	1095	8.3	99.5	35
Q5lpt4 silicibacte	2	714	8.1	96.5	36
Q37ik3 rhodopseuo	2	493	8.0	95.5	37
Q30sk2 thiomicrosp	2	616	7.9	95	38
Q9uzw1 pyrococcus	2	424	7.8	93.5	39
Q60hh0 macaca fasc	2	438	7.8	93.5	40
Q8ho10 thrips imag	2	564	7.8	93.5	41
Q2ix08 rhodopseuo	2	304	7.7	92.5	42
Q3d2j8 streptococc	2	651	7.7	92	43
Q8du10 streptococc	2	246	7.6	91	44
Q7vft4 helicobacte	2	525	7.6	91	45
Q3d8x6 streptococc	2	651	7.6	91	46
Q3duy5 streptococc	2	651	7.6	91	47
Q3klb2 streptococc	2	651	7.6	91	48
Q8dzo streptococc	2	651	7.6	91	49
Q8esmo streptococc	2	651	7.6	91	50
Q7nbj4 mycoplasma	2	262	7.6	90.5	51
Q3wyl1 rubrobacter	2	284	7.6	90.5	52
Q54f03 dictyosteli	2	530	7.6	90.5	53
Q36vr4 rhodopseuo	2	401	7.5	90	54
Q02038 cyanea capi	2	1911	7.5	89.5	55
Q6jct3 aleurodicus	2	233	7.5	89.5	56
Q8heh8 varroa dest	2	367	7.5	89.5	57
Q6jct6 aleurodicus	2	376	7.5	89.5	58
Q60ln0 caenorhabdi	2	478	7.5	89.5	59
Q84w7 streptococc	2	488	7.5	89.5	60
Q7rtb5 plasmodium	2	373	7.4	89	61
Q568r5 brachydanio	2	387	7.4	89	62
Q3dlx9 streptococc	2	651	7.4	89	63
Q4yc11 plasmodium	2	912	7.4	89	64
Q6wnv4 rana catesb	2	384	7.4	88.5	65
Q4cl73 crocosphaer	2	453	7.4	88	66
Q60qu6 caenorhabdi	2	755	7.4	88	67
Q4hdv8 campylobact	2	396	7.3	87.5	68
Q5zm65 gallus gall	2	473	7.3	87.5	69
Q3kqh5 xenopus lae	2	301	7.3	87	70
Q640e5 xenopus lae	2	304	7.3	87	71
Q7rrb2 plasmodium	2	610	7.3	87	72
Q6gn42 xenopus lae	2	707	7.3	87	73
Q8pym2 methanosaec	2	720	7.3	87	74
Q55ij0 cryptococcu	2	756	7.3	87	75
Q7nll9 gloeobacter	2	328	7.2	86.5	76
Q7z205 caenorhabdi	2	626	7.2	86.5	77
Q4ys44 plasmodium	2	647	7.2	86.5	78
Q2rix6 moorella th	2	891	7.2	86.5	79
Q87lg6 neurospora	2	613	7.2	86	80
Q787lg6 neurospora	2	1050	7.2	86	81
Q787lg6 neurospora	2	1056	7.2	86	82
Q4par7 utiilago ma	2	1453	7.2	86	83
Q4s220 tetraodon n	2	2515	7.2	86	84
P97067 salmonella	2	174	7.2	85.5	85
Q2up48 aspergillus	2	331	7.2	85.5	86
Q95086 homo sapien	2	336	7.2	85.5	87
Q4y634 plasmodium	2	337	7.2	85.5	88
Q95089 homo sapien	2	339	7.2	85.5	89
Q2ta70 homo sapien	2	360	7.2	85.5	90
Q9pme5 campylobact	2	396	7.2	85.5	91
Q13286 homo sapien	2	438	7.2	85.5	92
Q54949 homo sapien	2	438	7.2	85.5	93
Q47h59 decholoromon	2	438	7.2	85.5	94
P48651 homo sapien	2	473	7.2	85.5	95
Q2khy9 bos taurus	2	747	7.2	85.5	96
Q93gl8 salmonella	2	747	7.2	85.5	97
Q35hj0 bradyrhizob	2	302	7.1	85	98
Q9sf17 arabidopsis	2	348	7.1	85	99
Q6i2c1 bacillus an	2	377	7.1	85	100
Q51531 borrelia bu	2	448	7.1	85	101
Q82g38 streptomyce	2	797	7.1	85	102
Q4b5q6 polaromonas	2	2793	7.1	85	103
Q4itl6 azotobacter	2	412	7.1	84.5	104

105	84.5	7.1	430	2	Q5ZTB7_LEGPH	Q5ZTB7 legionella	178	82	6.9	201	2	Q45PV3_9CAUD	Q45PV3 bacterioph
106	84.5	7.1	471	1	PTSS1_CRIGR	Q00576 cricetulus	179	82	6.9	228	2	Q5E508_VIBF1	Q5E508 vibrio fisc
107	84.5	7.1	473	1	PTSS1_MOUSE	Q991h2 mus musculus	180	82	6.9	301	2	Q8RL23_HAEJA	Q8RL23 haemophilus
108	84.5	7.1	473	1	Q3UV14_MOUSE	Q3uv14 mus musculus	181	82	6.9	303	2	Q89L18_HAEJA	Q89L18 bradyrhizob
109	84.5	7.1	473	2	Q5POL5_RAT	Q5pol5 rattus norv	182	82	6.9	316	2	Q61RL6_CABER	Q61RL6 caenorhabd
110	84.5	7.1	487	2	Q6AOE5_MOUSE	Q6aoe5 mus musculus	183	82	6.9	382	2	Q5OHS8_PORGI	Q5OHS8 porphyromon
111	84.5	7.1	620	2	Q3Q9T9_9GAMM	Q3q9t9 shewanella	184	82	6.9	384	2	Q5OHU1_PORGI	Q5OHU1 porphyromon
112	84.5	7.1	886	2	Q2RANI_ORISA	Q2rani oryza sativ	185	82	6.9	387	2	Q3OPJ9_THIDN	Q3OPJ9 thiomicrosp
113	84.5	7.1	892	2	Q9JF90_VACCT	Q9jf90 vaccinia vi	186	82	6.9	461	2	Q6AHB8_LEIXX	Q6AHB8 leifsonia x
114	84.5	7.1	895	2	Q2TWS5_ASPOR	Q2twes aspergillus	187	82	6.9	472	2	Q7OJ50_HABIN	Q7OJ50 haemophilus
115	84.5	7.1	1118	2	Q65U88_MANSM	Q65u88 manheimia	188	82	6.9	564	2	Q2UHP4_ASPOR	Q2uhp4 aspergillus
116	84.5	7.1	3848	2	Q5CUX5_CRYPV	Q5cux5 cryptospori	189	82	6.9	581	2	Q4RQNS_TETNG	Q4rqns tetraodon n
117	84	7.0	396	2	Q5HSR1_CAMTR	Q5hsr1 campylobact	190	82	6.9	587	2	Q6C0H8_YAROW	Q6C0H8 yarrowia li
118	84	7.0	468	2	Q4Z8Z8_DESHA	Q4z8z8 desulfitoba	191	82	6.9	589	1	RGP1_MOUSE	RGP1 mus musculus
119	84	7.0	469	2	Q9JHK8_THEAC	Q9jhk8 thermoplas	192	82	6.9	589	2	Q8NZB5_MOUSE	Q8nzb5 m rangapl p
120	84	7.0	493	2	Q7TSH7_MOUSE	Q7tsh7 m potassium	193	82	6.9	589	2	Q8CZB3_MOUSE	Q8cze3 mus musculus
121	84	7.0	809	2	Q43RP5_SOLUS	Q43rp5 solibacter	194	82	6.9	589	2	Q91YS2_MOUSE	Q91ys2 mus musculus
122	84	7.0	1700	2	Q75JN1_DICTDI	Q75jn1 dictyosteli	195	82	6.9	646	2	Q6ZPH4_MOUSE	Q6zph4 mus musculus
123	83.5	7.0	170	2	Q4YS32_PLABE	Q4ys32 plasmodium	196	82	6.9	647	2	Q8PXU3_METMA	Q8pxu3 methanosarc
124	83.5	7.0	275	2	Q8XIT3_CLOPE	Q8xit3 clostridium	197	82	6.9	647	2	Q4HJ13_CAMLA	Q4hj13 campylobact
125	83.5	7.0	276	2	Q4D766_TRYCR	Q4d766 trypanosoma	198	82	6.9	819	2	Q4JCD0_SULAC	Q4jcd0 sulfolobus
126	83.5	7.0	303	2	Q6FNB8_CANGA	Q6fnb8 candida gla	199	82	6.9	989	2	Q8CDE6_YARLI	Q8cde6 yarrowia li
127	83.5	7.0	322	2	Q8LB40_ARATH	Q8lb40 arabidopsis	200	82	6.9	1031	2	Q8I564_PLAF7	Q8i564 plasmodium
128	83.5	7.0	352	2	Q97KT1_CLOAB	Q97kt1 clostridium	201	82	6.9	1466	2	P78576_EMENI	P78576 emericella
129	83.5	7.0	355	2	Q6KI24_MYCMA	Q6ki24 mycoplasma	202	82	6.9	1466	2	Q5AS02_EMENI	Q5as02 aspergillus
130	83.5	7.0	380	2	Q97C55_THEVO	Q97c55 thermoplas	203	81.5	6.8	190	2	Q9KIA9_ECOLI	Q9kia9 escherichia
131	83.5	7.0	429	2	Q5E5F1_VIBF1	Q5e5f1 vibrio fisc	204	81.5	6.8	287	2	Q5ID23_ENTHI	Q5id23 entamoeba h
132	83.5	7.0	490	2	Q9CTA9_MOUSE	Q9cta9 mus musculus	205	81.5	6.8	293	2	Q9B893_9TREM	Q9b893 schistosoma
133	83.5	7.0	503	2	Q36S46_MARRY	Q36s46 marinobacte	206	81.5	6.8	306	2	Q2X2A4_9GAMM	Q2x2a4 shewanella
134	83.5	7.0	599	2	Q6PCX2_MOUSE	Q6pcx2 mus musculus	207	81.5	6.8	306	2	Q2ZSH6_SHEPU	Q2zsh6 shewanella
135	83.5	7.0	662	2	Q88P20_PSEPK	Q88p20 pseudomonas	208	81.5	6.8	311	2	Q8CDI4_MOUSE	Q8cdi4 mus musculus
136	83.5	7.0	834	2	Q9JHF5_MOUSE	Q9jhf5 mus musculus	209	81.5	6.8	342	2	Q3Z083_9GAMM	Q3z083 uncultured
137	83.5	7.0	834	2	Q9JL12_MOUSE	Q9jl12 mus musculus	210	81.5	6.8	349	1	RNFD_PASMU	RNFD pasteurellia
138	83.5	7.0	834	2	Q91W06_MOUSE	Q91w06 mus musculus	211	81.5	6.8	352	2	Q9H7E5_HUMAN	Q9h7e5 homo sapien
139	83.5	7.0	1034	2	Q7Z2B9_TRYCR	Q7z2b9 trypanosoma	212	81.5	6.8	387	2	Q7ZCJ7_DESVH	Q7zcj7 desulfovibr
140	83.5	7.0	2483	2	Q5CH29_CRYHO	Q5ch29 cryptospori	213	81.5	6.8	391	2	Q4VBD2_MOUSE	Q4vbd2 mus musculus
141	83	6.9	238	2	Q6YR96_ONYPE	Q6yr96 onion yello	214	81.5	6.8	414	2	Q6PAH4_MOUSE	Q6pah4 mus musculus
142	83	6.9	248	2	Q8GCS6_EUBAC	Q8gcs6 eubacterium	215	81.5	6.8	438	2	Q35934_MOUSE	Q35934 mus musculus
143	83	6.9	280	2	Q3JED6_NITOC	Q3jed6 nitrosococc	216	81.5	6.8	438	2	Q8C5B1_MOUSE	Q8c5b1 mus musculus
144	83	6.9	291	2	Q8ZD70_YERPE	Q8zdt0 yersinia pe	217	81.5	6.8	447	2	Q7VRC0_BIOFL	Q7vrc0 blochmannia
145	83	6.9	438	2	Q5XIH8_RAT	Q5xih8 rattus norv	218	81.5	6.8	463	2	Q4ELJ5_LISMO	Q4elj5 listeria mo
146	83	6.9	589	2	Q7TWM1_MOUSE	Q7twm1 mus musculus	219	81.5	6.8	465	2	Q8Q3C9_BRARE	Q8q3c9 brachydanio
147	83	6.9	590	2	Q34192_CRION	Q34192 crithidia o	220	81.5	6.8	519	2	Q9NVS8_HUMAN	Q9nvs8 homo sapien
148	83	6.9	738	2	Q3OS24_THIDN	Q3os24 thiomicrosp	221	81.5	6.8	577	2	Q6PI26_HUMAN	Q6pi26 homo sapien
149	83	6.9	1056	2	Q8C2V1_MOUSE	Q8c2v1 mus musculus	222	81.5	6.8	577	2	Q7Z748_HUMAN	Q7z748 homo sapien
150	83	6.9	1388	2	Q5UD28_MOUSE	Q5ud28 mus musculus	223	81.5	6.8	645	2	Q67UQ9_ORISA	Q67uq9 oryza sativ
151	83	6.9	2661	2	Q7RMS4_PLAYO	Q7rms4 plasmodium	224	81.5	6.8	716	2	Q8DLB4_SYNEL	Q8dlb4 synechococc
152	82.5	6.9	174	2	P97231_9ENTR	P97231 salmonella	225	81.5	6.8	735	2	Q6B3Y6_ECOLI	Q6b3y6 escherichia
153	82.5	6.9	186	1	TRAS2_ECOLI	P14498 escherichia	226	81.5	6.8	892	2	Q775R6_CAMPS	Q775r6 camelpox vi
154	82.5	6.9	186	2	Q7BBW2_SALTI	Q7bbw2 salmonella	227	81.5	6.8	892	2	Q8V2P5_CAMPM	Q8v2p5 ashbaya goss
155	82.5	6.9	218	2	Q3IQR1_NATPD	Q3iqr1 natronomoma	228	81.5	6.8	1092	2	Q755K6_ASHGO	Q755k6 tetraodon n
156	82.5	6.9	239	1	Y247_MTCGE	P47489 mycoplasma	229	81.5	6.8	1472	2	Q4SGQ6_TETNG	Q4sgq6 tetraodon n
157	82.5	6.9	239	2	Q36E00_9GAMM	Q36e00 shewanella	230	81.5	6.8	1480	2	Q7R386_GZALA	Q7r386 giardia lam
158	82.5	6.9	341	2	Q56918_YERIN	Q56918 yersinia en	231	81.5	6.8	1659	2	Q5KGP3_CRYNE	Q5kgp3 cryptococcu
159	82.5	6.9	367	2	Q8HCK3_9ACNR	Q8hck3 varroa dest	232	81.5	6.8	1692	2	Q5SS96_CRYNE	Q5ss96 cryptococcu
160	82.5	6.9	389	2	Q5FL80_LACAC	Q5fl80 lactobacill	233	81	6.8	216	2	Q2NFK6_9EURY	Q2nfq6 methanocospa
161	82.5	6.9	406	2	Q87249_9LACT	Q87249 lactococccu	234	81	6.8	285	2	Q2KI24_BORAV	Q2ky24 bordetella
162	82.5	6.9	419	2	Q19134_RABIT	Q19134 cryotolagus	235	81	6.8	385	2	Q9ZQ69_ARATH	Q9zq69 arabidopsis
163	82.5	6.9	422	2	Q333G1_9CAUD	Q333g1 bacterioph	236	81	6.8	410	2	Q6D043_ERWCT	Q6d043 erwinia car
164	82.5	6.9	471	2	Q9QW77_CRIGR	Q9qw77 cricetulus	237	81	6.8	483	2	Q4MPN6_BACCE	Q4mpn6 bacillus ce
165	82.5	6.9	510	2	Q95OM6_9FUNG	Q95om6 rhizophydiu	238	81	6.8	486	2	Q63ET7_BACCE	Q63et7 bacillus ce
166	82.5	6.9	604	2	Q8RHM3_FUSNG	Q8rhj3 fusobacteri	239	81	6.8	492	2	Q5A405_CANAL	Q5a405 candida alb
167	82.5	6.9	717	1	TRAD1_ECOLI	P09130 escherichia	240	81	6.8	510	2	Q5ALJ4_CANAL	Q5alj4 candida alb
168	82.5	6.9	781	2	Q4U8E8_THEAN	Q4u8e8 theileria a	241	81	6.8	520	1	YOU1_CABEL	YOU1 caenorhabd
169	82.5	6.9	891	2	Q57223_9POXV	Q57223 vaccinia vi	242	81	6.8	532	1	YHB7_YEAST	YHB7 trichodesmi
170	82.5	6.9	891	2	Q49P11_9POXV	Q49p11 vaccinia vi	243	81	6.8	780	2	Q8XSV5_RALSO	Q8xsv5 ralestonia s
171	82.5	6.9	891	2	Q6J3A9_9POXV	Q6j3a9 vaccinia vi	244	81	6.8	805	2	Q8XSV5_9HEPC	Q8xsv5 hepatitis c
172	82.5	6.9	891	2	Q80DW2_COMXP	Q80dw2 cowpox viru	245	81	6.8	3010	2	P97066_9ENTR	P97066 salmonella
173	82.5	6.9	892	2	Q6RZH3_9POXV	Q6rzh3 rabbitpox v	246	80.5	6.7	174	2	Q8TNE9_METAC	Q8tne9 aster yello
174	82.5	6.9	894	2	Q8QM00_COMXP	Q8qm00 cowpox viru	247	80.5	6.7	240	2	Q2NIM4_9MOLU	Q2nim4 methanosarc
175	82.5	6.9	1022	2	Q88V00_LACPL	Q88v00 lactobacill	248	80.5	6.7	242	2	Q8TNE9_METAC	Q8tne9 methanosarc
176	82	6.9	156	2	Q81501_9HEPC	Q81501 hepatitis c	249	80.5	6.7	284	2	Q3PSH1_NITHA	Q3psh1 nitrobacter
177	82	6.9	161	2	Q69UD2_ORISA	Q69ud2 oryza sativ	250	80.5	6.7	322	2	Q56WV6_ARATH	Q56wv6 arabidopsis

251	80.5	6.7	322	2	Q9SNE5_ARATH	Q9sne5	arabidopsis	324	79.5	6.7	307	2	Q89NC2_BRAJA	Q89nc2	bradyrhizob
252	80.5	6.7	353	1	MTRIA_PROSU	P49217	rhodopus eu	325	79.5	6.7	367	2	Q8ESY3_OCEIH	Q8esy3	oceanobacil
253	80.5	6.7	366	2	Q86KB8_DICDI	Q86kt8	dichytosteli	326	79.5	6.7	379	2	Q508J9_PERO	Q508j9	perognathus
254	80.5	6.7	396	1	BTNL_SCHPO	Q9us09	schizosacch	327	79.5	6.7	391	2	Q6TY96_9BILA	Q6ty96	xiphinema a
255	80.5	6.7	417	1	TNAL_PROVU	P28785	proteus vul	328	79.5	6.7	392	2	Q2MDL9_VIVIN	Q2mdl9	viverricula
256	80.5	6.7	423	2	Q4KL8B_STRPN	Q4kl8b	streptococc	329	79.5	6.7	404	2	Q405X5_9RHOB	Q405x5	jannaschula
257	80.5	6.7	463	2	Q722Q4_LISMF	Q722q4	listeria mo	330	79.5	6.7	438	1	CLN3_CANFA	Q29611	canis famil
258	80.5	6.7	463	2	Q8Y988_LISMO	Q8y988	listeria mo	331	79.5	6.7	463	2	Q92E13_LISIN	Q92e13	listeria in
259	80.5	6.7	463	2	Q5EA23_XENLA	Q5ea23	xenopus lae	332	79.5	6.7	468	2	Q30R92_THIDN	Q30r92	thiomicrosp
260	80.5	6.7	485	2	Q5A256_DICDI	Q5a256	dichytosteli	333	79.5	6.7	488	2	Q6QU70_ASPNG	Q6qu70	aspergillus
261	80.5	6.7	486	2	Q9G861_9EUKA	Q9g861	malawimonas	334	79.5	6.7	491	1	VIEL_HCMVT	P03169	human cytom
262	80.5	6.7	536	1	WVIN_CHLTR	Q46378	chlamydia t	335	79.5	6.7	546	1	FLVC2_RAT	P60815	rattus norv
263	80.5	6.7	536	1	Q3KL71_CHLTA	Q3kl71	chlamydia t	336	79.5	6.7	549	2	Q4Z2F3_PLABE	Q4z2f3	plasmodium
264	80.5	6.7	548	2	Q7RC45_PLAYO	Q7rc45	plasmodium	337	79.5	6.7	598	2	O51954_BORHE	O51954	borrelia he
265	80.5	6.7	554	2	Q4YGE4_PLACH	Q4yge4	human rotav	338	79.5	6.7	649	2	Q6B208_DEBHA	Q6b208	debaromyce
266	80.5	6.7	599	2	Q91ME6_9REOV	Q91me6	human rotav	339	79.5	6.7	674	2	Q86P19_DROME	Q86p19	drosophila
267	80.5	6.7	644	1	YNL5_YEAST	P53925	saccharomyc	340	79.5	6.7	688	2	Q35Y20_9GAMM	Q35y20	shewanella
268	80.5	6.7	644	1	Q6B2V3_YEAST	Q6b2v3	saccharomyc	341	79.5	6.7	688	2	Q2Z578_9GAMM	Q2z578	shewanella
269	80.5	6.7	716	2	Q5JBP7_ECOLI	Q5jbp7	escherichia	342	79.5	6.7	726	2	Q9EUJ3_SALFT	Q9euJ3	salmonella
270	80.5	6.7	732	2	Q2TU08_ECOLI	Q2tu08	escherichia	343	79.5	6.7	732	2	O5J497_SALCH	O5j497	salmonella
271	80.5	6.7	732	2	Q6SIZ5_ECOLI	Q6siz5	escherichia	344	79.5	6.7	748	2	Q4WB47_ASPFU	Q4wb47	aspergillus
272	80.5	6.7	733	2	Q3YTF2_SHISS	Q3ytf2	shigella so	345	79.5	6.7	784	2	Q9VYU0_DROME	Q9vyu0	drosophila
273	80.5	6.7	738	1	TRAD2_ECOLI	P22708	escherichia	346	79.5	6.7	784	2	Q8KDB0_CHLTE	Q8kdb0	chlorobium
274	80.5	6.7	738	1	Q7AK62_9ZZZZ	Q7ak62	plasmid r10	347	79.5	6.7	818	2	Q5HXC6_CAMJR	Q5hxc6	campylobact
275	80.5	6.7	891	1	VP4A_VACCC	P20642	vaccinia vi	348	79.5	6.7	886	2	Q4ALC7_9CHLB	Q4alc7	chlorobium
276	80.5	6.7	891	1	VP4A_VACCV	P16715	vaccinia vi	349	79.5	6.7	1708	2	Q4LE27_HUMAN	Q4le27	homo sapien
277	80.5	6.7	891	2	O51XQ4_MONPV	Q5ixq4	monkeypox v	350	79.5	6.7	3409	2	Q7SI27_NEUCR	Q7si27	neutrospora
278	80.5	6.7	891	2	Q76ZQ5_9POXV	Q76zq5	vaccinia vi	351	79	6.6	1114	2	Q6VRR6_HELPY	Q6vrr6	helicobacte
279	80.5	6.7	891	2	Q8V4W5_MONPV	Q8v4w5	monkeypox v	352	79	6.6	238	2	Q3UWH0_MOUSE	Q3uwh0	m 15 days e
280	80.5	6.7	955	2	Q2UU23_ASPOR	Q2uu23	aspergillus	353	79	6.6	251	2	Q6M0I2_METMP	Q6m0i2	methanococc
281	80.5	6.7	955	2	Q7SC49_NEUCR	Q7sc49	neutrospora	354	79	6.6	288	2	Q3EEL5_ACTSC	Q3eel5	actinobacil
282	80.5	6.7	1687	2	Q9ZT82_ARATH	Q9zt82	arabidopsis	355	79	6.6	300	2	Q80ZH3_9MURI	Q80zh3	arvicanthis
283	80	6.7	103	2	Q9RX39_DEIRA	Q9rx39	deinococcus	356	79	6.6	312	2	Q8RCM6_FUSNN	Q8rcm6	fusobacteri
284	80	6.7	156	2	Q81513_9HEPC	Q81513	hepatitis c	357	79	6.6	308	2	Q6KH29_MYCNO	Q6kh29	mycoplasma
285	80	6.7	197	2	Q7YWX2_CAEL	Q7ywx2	caenorhabdi	358	79	6.6	323	2	Q7KSI9_DROME	Q7ksi9	drosophila
286	80	6.7	238	2	Q5QTD8_HUMAN	Q5qtd8	homo sapien	359	79	6.6	345	1	RNFD_BUCAP	Q360Y1	shewanella
287	80	6.7	238	2	O5QKH1_MACFA	Q95kh1	macaca fasc	360	79	6.6	349	1	RNFD_BUCAP	Q8ka19	buchnera ap
288	80	6.7	255	2	Q6V7H6_EAV	Q6v7h6	equine arte	361	79	6.6	350	2	Q36R10_MARHY	Q36r10	marinobacte
289	80	6.7	280	2	Q4MTK3_BACCE	Q4mtk3	bacillus ce	362	79	6.6	356	2	O5X814_LEGPA	O5x814	legionella
290	80	6.7	280	2	Q63SR8_BACCC	Q63sr8	bacillus ce	363	79	6.6	356	2	Q7MG43_VIBVY	Q7mg43	vibrio vuln
291	80	6.7	280	2	Q6HEF5_BACHK	Q6hef5	bacillus th	364	79	6.6	375	2	Q4ZXH6_PSEU2	Q4zxh6	pseudomonas
292	80	6.7	280	2	Q819H0_BACCR	Q8e19h0	bacillus ce	365	79	6.6	375	2	Q887L9_PSESM	Q887l9	pseudomonas
293	80	6.7	280	2	Q731V3_BACCI	Q731v3	bacillus ce	366	79	6.6	428	2	Q2ZGP3_CALSA	Q2zgp3	caldicellul
294	80	6.7	280	2	Q81MM0_BACAN	Q81mm0	bacillus an	367	79	6.6	466	2	Q2JTY0_9CVAN	Q2jty0	cyanobacter
295	80	6.7	290	2	Q7ASV6_STAAN	Q7asv6	staphylococ	368	79	6.6	484	2	Q6NIE0_CORDI	Q6nie0	corynebacte
296	80	6.7	290	2	Q99UM2_STAAM	Q99um2	staphylococ	369	79	6.6	770	2	O5LA24_BACFN	O5la24	bacteroides
297	80	6.7	296	2	Q3EEG9_ACTSC	Q3ee9	actinobacil	370	79	6.6	828	2	Q64QD3_BACFN	Q64qd3	bacteroides
298	80	6.7	300	2	Q9C840_ARATH	Q9c840	arabidopsis	371	79	6.6	1232	2	Q4RGA8_TETNG	Q4rga8	tetraodon n
299	80	6.7	309	1	RTM1_YEAST	P40113	saccharomyc	372	79	6.6	1232	2	Q3JBT9_NITOC	Q3jbt9	nitrosococc
300	80	6.7	343	2	Q7USB9_RHOBA	Q7usb9	rhodopitell	373	79	6.6	1531	2	Q96L95_HUMAN	Q96l95	homo sapien
301	80	6.7	347	2	Q9FPM1_ARATH	Q9fpm1	arabidopsis	374	79	6.6	1679	2	Q86TB3_HUMAN	Q86tb3	homo sapien
302	80	6.7	355	2	Q73JAS_TREDE	Q73jas	treponema d	375	79	6.6	1780	2	Q61T87_CABER	Q61t87	caenorhabdi
303	80	6.7	359	2	Q7N4F8_PHOLL	Q7n4f8	photorhabdu	376	79	6.6	2751	2	Q4Y3S8_PLACH	Q4y3s8	plasmodium
304	80	6.7	360	2	Q9H1X3_HUMAN	Q9h1x3	homo sapien	377	79	6.6	3010	2	Q9Q3H8_9HEPC	Q9q3h8	hepatitis c
305	80	6.7	388	2	O58427_PYRHO	O58427	pyrococcus	378	79	6.6	229	2	Q353U9_9GAMM	Q353u9	alkalilimni
306	80	6.7	418	2	Q3P007_9GAMM	Q3p007	shewanella	379	78.5	6.6	232	2	Q466U5_METBA	Q466u5	methanosarc
307	80	6.7	488	2	Q650S8_ORYSA	Q650s8	oryza sativ	380	78.5	6.6	232	1	Y350_MTCPN	P75428	mycoplasma
308	80	6.7	540	2	Q6FXI7_CANGA	Q6fxi7	candida gla	381	78.5	6.6	239	1	Q4Z3F6_PLABE	Q4z3f6	plasmodium
309	80	6.7	554	2	Q4PC93_USTWA	Q4pc93	ustilago ma	382	78.5	6.6	263	2	Q5IPE7_9RODE	Q5ipe7	perognathus
310	80	6.7	650	2	Q699F8_ANOGA	Q699f8	anopheles g	383	78.5	6.6	266	2	Q92DL5_LISIN	Q92dl5	listeria in
311	80	6.7	661	2	Q759V6_ASHGO	Q759v6	ashbya goss	384	78.5	6.6	269	2	Q92DM5_LISIN	Q92dm5	mesorhizobi
312	80	6.7	680	2	Q7VH08_HELHP	Q7vh08	helicobacte	385	78.5	6.6	272	2	Q3WQW4_9RHIZ	Q3wqw4	mesorhizobi
313	80	6.7	700	2	Q4EKL7_LISMO	Q4ekl7	listeria mo	386	78.5	6.6	292	2	O5V6V4_HALMA	O5v6v4	haloarcula
314	80	6.7	700	2	Q720Z1_LISMF	Q720z1	listeria mo	387	78.5	6.6	305	2	Q374B4_RHOPA	Q374b4	rhodopsendo
315	80	6.7	700	2	Q4I7J8_GIBZE	Q4i7j8	gibberella	388	78.5	6.6	306	2	Q345Q5_RHOPA	Q345q5	rhodopsendo
316	80	6.7	893	2	Q9Q1Y9_9HEPC	Q9q1y9	hepatitis c	389	78.5	6.6	313	2	Q9LOB3_STRCO	Q9lob3	streptomyce
317	79.5	6.7	266	2	Q3SLE7_THIDA	Q3sle7	thiobacillu	390	78.5	6.6	353	2	Q4HJT2_CAMLA	Q4hjt2	campylobact
318	79.5	6.7	266	2	Q51PF8_9RODE	Q51pf8	perognathus	391	78.5	6.6	358	1	RNFD_HAEIN	Q57288	haemophilus
319	79.5	6.7	266	2	Q51PF9_9RODE	Q51pf9	perognathus	392	78.5	6.6	358	2	Q4QJ05_HAEI8	Q4qj05	haemophilus
320	79.5	6.7	269	2	Q4EFC5_LISMO	Q4efc5	listeria mo	393	78.5	6.6	366	2	Q4EUI1_LISMO	Q4eui1	listeria mo
321	79.5	6.7	269	2	Q722B0_LISMF	Q722b0	listeria mo	394	78.5	6.6	380	2	Q8A8F8_BACTN	Q8a8f8	bacteroides
322	79.5	6.7	273	2	Q3WS44_9RHIZ	Q3ws44	mesorhizobi	395	78.5	6.6	382	2	O5LE17_BACFN	O5le17	bacteroides
323	79.5	6.7	304	2	Q33ZM2_RHOPA	Q33zm2	rhodopsendo	396	78.5	6.6	382	2	Q64V54_BACFR	Q64v54	bacteroides

397	78.5	6.6	418	2	Q65LP8_BACLD	Q65LP8 bacillus li	470	77.5	6.5	299	2	Q8ZAL1_YERPE	Q8Zall1 yersinia pe
398	78.5	6.6	451	2	Q65UD5_MANSM	Q65uds5 manheimia	471	77.5	6.5	310	2	Q8DL16_YERPE	Q8dl16 yersinia pe
399	78.5	6.6	471	1	5HT2A_CRIGR	P18599 cricetulus	472	77.5	6.5	327	2	Q9PQGI_UREPD	Q9pqgi1 ureaplasma
400	78.5	6.6	512	2	Q8GID7_BRUSU	Q8gid7 brucella su	473	77.5	6.5	328	2	Q9K686_BACHD	Q9k686 bacillus ha
401	78.5	6.6	538	2	Q4HFB8_CAMCO	Q4hfb8 campylobact	474	77.5	6.5	338	2	Q42882_SCHPO	Q42882 schizosacch
402	78.5	6.6	546	2	Q3TL16_RAT	Q3tl16 rattus norv	475	77.5	6.5	347	2	Q4AFU3_9CHLB	Q4afu3 chlorobium
403	78.5	6.6	557	2	Q5CXU4_CRYPV	Q5cxu4 cryptospori	476	77.5	6.5	365	2	Q8R770_THETN	Q8r770 thermoanaer
404	78.5	6.6	587	2	Q3D365_STRAG	Q3d365 streptococc	477	77.5	6.5	377	2	Q4R1V7_VARHI	Q4r1v7 vargula hil
405	78.5	6.6	609	2	Q3DHN0_STRAG	Q3dhn0 streptococc	478	77.5	6.5	377	2	Q4R1X9_VARHI	Q4r1x9 vargula hil
406	78.5	6.6	666	1	KUP_STRAS5	Q8dnl1 streptococc	479	77.5	6.5	377	2	Q4R264_VARHI	Q4r264 vargula hil
407	78.5	6.6	666	2	Q3DMX9_STRAG	Q3dmx9 streptococc	480	77.5	6.5	377	2	Q4R2A7_VARHI	Q4r2a7 vargula hil
408	78.5	6.6	666	2	Q3K107_STRAL	Q3k107 streptococc	481	77.5	6.5	377	2	Q4R2P5_VARHI	Q4r2p5 vargula hil
409	78.5	6.6	678	2	Q61710_MOUSE	Q61710 mus sapien	482	77.5	6.5	377	2	Q4R2P6_VARHI	Q4r2p6 vargula hil
410	78.5	6.6	681	2	Q769F3_HUMAN	Q769f3 homo sapien	483	77.5	6.5	379	2	Q4R2P5_VARHI	Q4r2p5 vargula hil
411	78.5	6.6	683	2	Q769F4_HUMAN	Q769f4 homo sapien	484	77.5	6.5	384	2	Q4R2P5_VARHI	Q4r2p5 vargula hil
412	78.5	6.6	689	2	Q3Q502_9GAMM	Q3q502 shewanella	485	77.5	6.5	392	2	Q8WUY0_CLOBE	Q8wuy0 clostridium
413	78.5	6.6	726	2	Q4UC59_THEAN	Q4uc59 theileria a	486	77.5	6.5	411	2	Q9P6N5_SCHPO	Q9p6n5 schizosacch
414	78.5	6.6	766	1	ABCB9_HUMAN	Q9np78 homo sapien	487	77.5	6.5	416	2	Q4YTQ0_PLABE	Q4ytq0 plasmodium
415	78.5	6.6	769	2	Q6P2Q0_HUMAN	Q6p2q0 homo sapien	488	77.5	6.5	422	2	Q9HKX6_THEAC	Q9hkk6 thermoplasm
416	78.5	6.6	796	2	Q5W9G7_HUMAN	Q5w9g7 homo sapien	489	77.5	6.5	430	2	Q5WUJ7_LSGPL	Q5wu77 legionella
417	78.5	6.6	867	2	Q4N908_THEPA	Q4n908 theileria p	490	77.5	6.5	440	2	Q9YI23_PEDMN	Q9zy23 pedionomas
418	78.5	6.6	1308	2	Q4XVA2_PLACH	Q4xva2 plasmodium	491	77.5	6.5	458	2	Q62XT1_BACLD	Q62xt1 bacillus li
419	78.5	6.6	1473	2	Q8IKH9_PLAF7	Q8ikh9 plasmodium	492	77.5	6.5	481	2	Q4P6B0_USTMA	Q4p6b0 ustilago ma
420	78	6.5	188	2	Q81YM2_BACAN	Q81ym2 bacillus an	493	77.5	6.5	483	2	Q9G8V8_9CRYP	Q9g8v8 rhodomonas
421	78	6.5	219	2	Q8W2Y0_ORYSA	Q8w2y0 oryza sativ	494	77.5	6.5	491	2	Q28284_9CRYP	Q28284 archaeoglob
422	78	6.5	226	2	Q7T829_9CORO	Q7t829 infectious	495	77.5	6.5	491	2	Q6SX10_HCMV	Q6sx10 human cytom
423	78	6.5	240	2	Q9CFP6_PASMU	Q9cfp6 pasteurella	496	77.5	6.5	512	2	Q57DX0_BRUAB	Q57dx0 brucella ab
424	78	6.5	245	2	P94625_CLODI	P94625 clostridium	497	77.5	6.5	512	2	Q8YGI2_BRUAB	Q8ygi2 brucella me
425	78	6.5	252	2	Q6B8K2_GRATL	Q6b8k2 gracilaria	498	77.5	6.5	512	2	Q3YNB5_BRUA2	Q3ynb5 brucella ab
426	78	6.5	259	2	Q9KD13_BACHD	Q9kd13 bacillus ha	499	77.5	6.5	526	2	Q3VJ85_9CHLB	Q3vj85 pelliciotyon
427	78	6.5	298	2	Q4B8H2_PSE14	Q4b8h2 pseudomonas	500	77.5	6.5	538	2	Q4HPP2_CAMUP	Q4hpp2 campylobact
428	78	6.5	299	2	Q2KXZ7_BORAV	Q2kxz7 bordetella	501	77.5	6.5	543	2	Q2ZED8_CALSA	Q2zed8 caldicellul
429	78	6.5	321	2	Q96XC4_SULTO	Q96xc4 sulfobolus	502	77.5	6.5	548	2	Q2RIU9_ORYSA	Q2riu9 oryza sativ
430	78	6.5	339	2	Q8D4K9_VIBVU	Q8d4k9 vibrio vuln	503	77.5	6.5	556	2	Q89180_VARV	Q89180 variola vir
431	78	6.5	345	2	Q2ZAV5_9GAMM	Q2zav5 shewanella	504	77.5	6.5	556	2	Q89232_VARV	Q89232 variola vir
432	78	6.5	357	2	Q5BJW9_RAT	Q5bjw9 rattus norv	505	77.5	6.5	567	2	Q7RNK0_PLAYO	Q7rnk0 plasmodium
433	78	6.5	360	2	Q95IA3_TETH	Q95ia3 tetrahymena	506	77.5	6.5	572	2	Q4XZG8_PLACH	Q4xzg8 plasmodium
434	78	6.5	382	2	Q97HC3_CLOAB	Q97hc3 clostridium	507	77.5	6.5	618	2	Q59P22_CANAL	Q59p22 candida alb
435	78	6.5	414	2	Q8TN61_METAC	Q8tn61 methanosarc	508	77.5	6.5	620	2	Q8EKA1_SHEON	Q8ekal shewanella
436	78	6.5	428	2	Q8D5Y9_VIBVU	Q8d5y9 vibrio vuln	509	77.5	6.5	654	2	Q3MXT8_9BELT	Q3mxt8 syntrophoba
437	78	6.5	431	2	Q9JRS0_ACTAC	Q9jrs0 actinobacil	510	77.5	6.5	676	2	Q4RUC9_TETNG	Q4ruc9 tetraodon n
438	78	6.5	442	2	Q7MD08_VIBVU	Q7md08 vibrio vuln	511	77.5	6.5	734	1	NUSC_ORYGA	P12129 oryza sativ
439	78	6.5	452	2	Q36DZ4_9GAMM	Q36dz4 shewanella	512	77.5	6.5	788	2	Q4K5I9_PSEF5	Q4k5i9 pseudomonas
440	78	6.5	471	1	Y872_HAEIN	Q57491 haemophilus	513	77.5	6.5	892	1	VP4A_VARV	P33817 variola vir
441	78	6.5	486	2	Q6HMA8_BACHK	Q6hma8 bacillus th	514	77.5	6.5	892	1	Q9QNI0_VARV	Q9qni0 variola min
442	78	6.5	494	2	Q3NGA0_9DELT	Q3nga0 syntrophoba	515	77.5	6.5	979	2	Q7MLV5_VIBVY	Q7mlv5 vibrio vuln
443	78	6.5	545	2	Q6FSM9_CANGA	Q6fsm9 candida gla	516	77.5	6.5	1033	2	Q5BL65_XENTR	Q5bl65 xenopus tro
444	78	6.5	638	2	Q2Z024_9CHLR	Q2z024 uncultured	517	77.5	6.5	1140	2	Q5CTR7_CRYPV	Q5ctr7 cryptospori
445	78	6.5	641	2	Q9LIC2_ARATH	Q9lic2 arabidopsis	518	77.5	6.5	1476	2	Q8ST66_DICDI	Q8st66 dictyosteli
446	78	6.5	650	2	Q2YZ60_STAAB	Q2yz60 staphylococ	519	77.5	6.5	1784	2	Q53377_LOLOP	Q53377 loligo opal
447	78	6.5	658	2	Q7QG08_ANOGA	Q7qg08 anopheles g	520	77.5	6.5	1959	2	Q5Z5B8_ORYSA	Q5z5b8 oryza sativ
448	78	6.5	688	2	Q98M77_RHTLO	Q98m77 rhizobium l	521	77.5	6.5	2141	2	Q869H2_LYMST	Q869h2 lynnaea sta
449	78	6.5	748	2	Q420Y8_DESHA	Q420y8 desulfitoba	522	77.5	6.5	6680	2	Q5CXT7_CRYPV	Q5cxt7 cryptospori
450	78	6.5	1042	2	Q3SDA8_PARTE	Q3sda8 paramecium	523	77	6.4	160	2	Q3EF80_ACTSC	Q3ef80 actinobacil
451	78	6.5	1088	2	Q43RR2_SOLUS	Q43rr2 solibacter	524	77	6.4	170	2	Q72UC4_LEPIC	Q72uc4 leptospira
452	78	6.5	1297	2	Q9Y817_SCHPO	Q9y817 schizosacch	525	77	6.4	170	2	Q8F0Q4_LEPIC	Q8foq4 leptospira
453	78	6.5	2136	1	YCF2_MARPO	P09975 marchantia	526	77	6.4	191	2	Q3VSI6_PROAE	Q3vei6 prosthecoch
454	78	6.5	7186	1	RIAB_CVMJH	P19751 m replicase	527	77	6.4	206	2	Q3LWE2_CHLS6	Q3lwe2 shewanella
455	77.5	6.5	176	2	Q976T7_SULTO	Q976t7 sulfobolus	528	77	6.4	226	2	Q33VA0_9GAMM	Q33va0 shewanella
456	77.5	6.5	190	2	Q9KIA8_ECOLI	Q9kia8 escherichia	529	77	6.4	249	2	Q2Z645_9GAMM	Q2z645 shewanella
457	77.5	6.5	263	2	Q4MQY0_BACCE	Q4mqy0 bacillus ce	530	77	6.4	255	2	Q98VN5_EAV	Q98vn5 equine arte
458	77.5	6.5	263	2	Q81I83_BACCR	Q81i83 bacillus ce	531	77	6.4	280	2	Q3EU30_BACTI	Q3eu30 bacillus th
459	77.5	6.5	263	2	Q73DX2_BACCI	Q73dx2 bacillus ce	532	77	6.4	286	2	Q6I082_BACAN	Q6i082 bacillus an
460	77.5	6.5	266	2	Q5IPF6_PERLO	Q5ipf6 perognathus	533	77	6.4	286	2	Q73A28_BACCI	Q73a28 bacillus ce
461	77.5	6.5	269	2	Q3EXW2_BACTI	Q3exw2 bacillus th	534	77	6.4	287	2	Q54LT2_DICDI	Q54lt2 dictyosteli
462	77.5	6.5	269	2	Q4EV75_LISNO	Q4ev75 listeria mo	535	77	6.4	288	2	Q3GB03_9FRIC	Q3gb03 syntrophomo
463	77.5	6.5	289	2	Q8Y8T5_LISNO	Q8y8t5 listeria mo	536	77	6.4	315	2	Q4HFE7_CAMCO	Q4hfe7 campylobact
464	77.5	6.5	270	2	Q8HIY1_PERLO	Q8hiy1 perognathus	537	77	6.4	332	2	Q9XTH3_CABEL	Q9xth3 caenorhadi
465	77.5	6.5	270	2	Q8HIY2_PERLO	Q8hiy2 perognathus	538	77	6.4	346	2	Q2NSZ8_SODGL	Q2nsz8 sodalis glo
466	77.5	6.5	270	2	Q8HIY3_PERLO	Q8hiy3 perognathus	539	77	6.4	353	1	MTE1A_MOUSE	Q61184 mus musculu
467	77.5	6.5	270	2	Q8HIY4_PERLO	Q8hiy4 perognathus	540	77	6.4	361	2	Q4EL37_LISMO	Q4el37 listeria mo
468	77.5	6.5	294	2	Q8ET30_OCEIH	Q8et30 oceanobacil	541	77	6.4	379	2	Q8WEK6_THOTA	Q8wek6 thomomys ta
469	77.5	6.5	299	2	Q66FT9_YERPS	Q66ft9 yersinia ps	542	77	6.4	383	2	Q8TZC2_METKA	Q8tzc2 methanopyru

543	77	6.4	386	2	Q7MXQ0	porphyromon	Q7mxq0	616	76.5	6.4	438	1	CLN3	MOUSE	Q61124	mus musculus
544	77	6.4	419	2	P94949	methanopyru	P94949	617	76.5	6.4	439	2	Q5LRQ8	BACFN	Q51bq8	bacteroides
545	77	6.4	423	2	Q71X88	listeria mo	Q71x88	618	76.5	6.4	439	2	Q64SN0	BACFR	Q64sn0	bacteroides
546	77	6.4	430	2	Q8U126	pyrococcus	Q8u126	619	76.5	6.4	451	2	Q660T8	BORGA	Q660t8	borrelia ga
547	77	6.4	435	2	Q73RD9	treponema d	Q73rd9	620	76.5	6.4	451	2	Q62GZ4	ORISA	Q62gz4	oryza sativ
548	77	6.4	444	2	Q6GD70	staphylococ	Q6gd70	621	76.5	6.4	463	2	Q82V00	NITEU	Q82v00	nitrosomona
549	77	6.4	444	2	Q8NYX5	staphylococ	Q8nyx5	622	76.5	6.4	468	1	YDEM	CABEL	Q19084	caenorhabdi
550	77	6.4	473	2	Q3GS79	psychobact	Q3gs79	623	76.5	6.4	468	2	Q3S1M1	CABEL	Q3s1m1	caenorhabdi
551	77	6.4	477	2	Q2SJS7	gamm	Q2sjs7	624	76.5	6.4	468	2	Q6SX39	HCW	Q6sx39	human cytom
552	77	6.4	481	2	Q4WQ93	aspergillus	Q4wq93	625	76.5	6.4	491	2	Q6SWP6	HCW	Q6swp6	human cytom
553	77	6.4	490	2	Q14670	homo sapien	Q14670	626	76.5	6.4	500	2	Q96ZH3	SULTO	Q96zh3	sulfolobus
554	77	6.4	491	2	Q9T251	phythothor	Q9t251	627	76.5	6.4	526	1	FLVC2	HUMAN	Q9up13	homo sapien
555	77	6.4	505	2	Q4UI56	theileria a	Q4ui56	628	76.5	6.4	526	2	Q53T9	HUMAN	Q53zt9	homo sapien
556	77	6.4	519	2	Q9ASQ7	arabidopsis	Q9asq7	629	76.5	6.4	528	2	Q7VP70	HAEDU	Q7vp70	haemophilus
557	77	6.4	537	2	Q518N5	entamoeba h	Q518n5	630	76.5	6.4	528	2	Q5HWZ4	CAMUR	Q5hwz4	campylobact
558	77	6.4	559	2	Q9AA4	caulobacter	Q9aa4	631	76.5	6.4	538	2	Q9PIV5	CAMJE	Q9piv5	campylobact
559	77	6.4	590	1	NUSM	trypanosoma	P04540	632	76.5	6.4	555	2	Q8N8G4	HUMAN	Q8nb94	homo sapien
560	77	6.4	606	2	Q2IFP2	9DELTA	Q2ifp2	633	76.5	6.4	560	2	Q627P1	CABER	Q627p1	caenorhabdi
561	77	6.4	616	2	Q5W2R7	SULTIS	Q5w2r7	634	76.5	6.4	570	2	Q7Z6J6	HUMAN	Q7z6j6	homo sapien
562	77	6.4	650	2	Q5HC06	STAAC	Q5hc06	635	76.5	6.4	584	2	Q2V4K0	ARATH	Q2v4k0	arabidopsis
563	77	6.4	650	2	Q6G633	STAAS	Q6g633	636	76.5	6.4	589	2	Q9ZLN1	HEUPJ	Q9zln1	helicobacte
564	77	6.4	650	2	Q6GDG1	STAAR	Q6gdg1	637	76.5	6.4	614	2	Q577U9	BRUAB	Q577u9	bruceella ab
565	77	6.4	650	2	Q7A374	STAAN	Q7a374	638	76.5	6.4	614	2	Q8FWB2	BRUAB	Q8fwb2	bruceella ab
566	77	6.4	650	2	Q8NUK4	STAAM	Q8nuk4	639	76.5	6.4	614	2	Q2YKG7	BRUAB	Q2ykg7	bruceella ab
567	77	6.4	722	2	Q632R1	BACCZ	Q632r1	640	76.5	6.4	615	2	Q5JF60	PYRKO	Q5jyf60	pyrococcus
568	77	6.4	738	2	Q8L838	ARATH	Q8l838	641	76.5	6.4	649	2	Q6KZL4	PICTO	Q6kzl4	picophilus
569	77	6.4	789	1	FTSK	STAAS	Q899t7	642	76.5	6.4	666	2	Q3DSN7	STRAG	Q3dsn7	streptococc
570	77	6.4	789	1	FTSK	STAAS	Q899t7	643	76.5	6.4	687	2	Q74520	SCHPO	Q74520	schizosacch
571	77	6.4	836	2	Q7Z1F2	PLAFA	Q7z1f2	644	76.5	6.4	773	2	Q8XN80	CLOPE	Q8xn80	clostridium
572	77	6.4	836	2	Q7Z1F2	PLAFA	Q7z1f2	645	76.5	6.4	775	2	Q4NGA4	THEPA	Q4nga4	theileria p
573	77	6.4	877	2	Q750H8	ASHGO	Q750h8	646	76.5	6.4	839	2	Q9I8C9	CHICK	Q9i8c9	gallus gall
574	77	6.4	991	2	Q81330	ARATH	Q81330	647	76.5	6.4	859	2	Q3XN69	9PROT	Q3xn69	magnetococc
575	77	6.4	1024	2	Q7Z1F1	PLAFA	Q7z1f1	648	76.5	6.4	902	2	Q4IIV8	GIBZE	Q4iiv8	giberella
576	77	6.4	1024	2	Q8IKZ6	PLAF7	Q8ikz6	649	76.5	6.4	909	2	Q54BU4	DICDI	Q54bu4	dicytyosteli
577	77	6.4	1025	2	Q25693	PLAFA	Q25693	650	76.5	6.4	909	2	Q8T9W6	DICDI	Q8t9w6	dicytyosteli
578	77	6.4	1117	2	Q9MI33	ARATH	Q9mi33	651	76.5	6.4	1034	2	Q4DWH6	TRYCR	Q4dwh6	trypanosoma
579	77	6.4	1137	2	Q4PG0	CHLLI	Q4pg0	652	76.5	6.4	1141	2	Q2RFN9	MOOTH	Q2rfn9	moorella th
580	77	6.4	1477	2	Q6FT99	CANGA	Q6ft99	653	76.5	6.4	1228	2	Q3NBS3	9PROT	Q3nbs3	nitrosomona
581	77	6.4	1500	2	Q9ZU94	ARATH	Q9zu94	654	76.5	6.4	1485	2	Q8EUA2	MYCPE	Q8eua2	mycoplasma
582	77	6.4	1814	2	Q6WH4	CABER	Q6wh4	655	76.5	6.4	1641	2	Q6BS27	DEBHA	Q6bs27	debaryomyce
583	77	6.4	3010	2	Q8I788	9HEPC	Q8i788	656	76	6.4	156	2	Q81504	9HEPC	Q81504	hepatitis c
584	77	6.4	3010	2	Q8I757	9HEPC	Q8i757	657	76	6.4	201	2	Q6MT09	MYCMS	Q6mt09	mycoplasma
585	77	6.4	3010	2	Q9J3G4	9HEPC	Q9j3g4	658	76	6.4	210	2	Q8PXL0	MEYMA	Q8pxl0	methanosarc
586	77	6.4	3013	2	Q6J6P5	9HEPC	Q6j6p5	659	76	6.4	255	2	Q6V715	EAV	Q6v715	equine arte
587	77	6.4	4416	2	Q9J3F3	SCORO	Q9j3f3	660	76	6.4	264	2	Q2LV10	9DELT	Q2lv10	syntrichus
588	77	6.4	4416	2	Q9J3F8	SCORO	Q9j3f8	661	76	6.4	292	2	Q8R7J2	THETN	Q8r7j2	thermonaer
589	77	6.4	7124	1	RIAB	CVW2	Q9pya3	662	76	6.4	292	2	Q8ELU4	OCEIH	Q8elu4	oceanobacil
590	76.5	6.4	189	2	Q3WS01	9RHIZ	Q3ws01	663	76	6.4	325	2	Q3B337	PELLID	Q3b337	pelodictyon
591	76.5	6.4	234	2	Q3W1W0	9ACTO	Q3w1w0	664	76	6.4	328	2	Q922H9	MESAU	Q922h9	mesocricetu
592	76.5	6.4	253	2	Q51PE6	PERLO	Q5ipe6	665	76	6.4	342	1	NU2M	LOEMI	Q4h7x1	deinococcus
593	76.5	6.4	266	2	Q51PE8	PERLO	Q5ipe8	666	76	6.4	346	2	Q4H7X1	9DETO	Q4h7x1	deinococcus
594	76.5	6.4	278	2	Q8XBFO	ECOS7	Q8xbfo	667	76	6.4	393	2	Q3LXK3	TARGR	Q3lrx3	taricha gra
595	76.5	6.4	281	2	Q8SKS9	9BILA	Q8sk9	668	76	6.4	402	2	Q21933	CABEL	Q21933	caenorhabdi
596	76.5	6.4	282	2	Q92WV5	RHIME	Q92wv5	669	76	6.4	425	2	Q9JRS2	ACTAC	Q9jrs2	actinobacil
597	76.5	6.4	342	1	YOE8	YEAST	Q8219	670	76	6.4	438	2	Q88HG7	PSPPK	Q88hg7	pyrrololatt
598	76.5	6.4	342	2	Q7Z250	CABEL	Q7z250	671	76	6.4	446	2	Q2Q1L3	9NSOP	Q2q1l3	grylloblatt
599	76.5	6.4	352	1	RNFD	SALTY	Q8268	672	76	6.4	461	2	Q85002	STRPN	Q85002	streptococc
600	76.5	6.4	352	1	RNFD	SALTY	Q8268	673	76	6.4	474	2	Q7ZSX4	LEPIC	Q7zsk4	leptospira
601	76.5	6.4	352	2	Q57P11	SALCH	Q57p11	674	76	6.4	474	2	Q8F2K0	LEPIN	Q8f2k0	leptospira
602	76.5	6.4	352	2	Q5PIC8	SALPA	Q5pic8	675	76	6.4	484	2	Q385J6	9TRYP	Q385j6	trypanosoma
603	76.5	6.4	358	2	Q3Y919	CRYGA	Q3y919	676	76	6.4	487	2	Q3ZEF8	EPFL	Q3zef8	epidermophy
604	76.5	6.4	379	1	CVB	DIFOR	Q9gav3	677	76	6.4	519	2	Q852P3	PERFR	Q852p3	perilla fru
605	76.5	6.4	379	2	Q3GBY7	OCHEPA	Q9gb7	678	76	6.4	567	2	Q6NXT6	HUMAN	Q6nxt6	homo sapien
606	76.5	6.4	379	2	Q508J3	9RODE	Q508j3	679	76	6.4	616	2	Q7QWH6	GIALA	Q7qwh6	giardia lam
607	76.5	6.4	379	2	Q508J5	PERLO	Q508j5	680	76	6.4	648	2	Q3MEJ3	ANAVT	Q3mej3	anabaena va
608	76.5	6.4	379	2	Q508L8	9RODE	Q508l8	681	76	6.4	669	2	Q9LZ27	ARATH	Q9lzt27	arabidopsis
609	76.5	6.4	380	2	Q8HN17	PRANA	Q8hn17	682	76	6.4	699	2	Q6IVM6	9GAMM	Q6ivm6	uncultured
610	76.5	6.4	387	2	Q3VX84	PROAE	Q3vx84	683	76	6.4	851	2	Q6CK04	KJULA	Q6ck04	kluyveromyc
611	76.5	6.4	391	2	Q4S129	TETNG	Q4s129	684	76	6.4	931	2	Q7NBN0	MYGGA	Q7nbn0	mycoplasma
612	76.5	6.4	395	2	Q8KHK2	ESAE	Q8khk2	685	76	6.4	953	2	Q5Z570	ORISA	Q5z570	oryza sativ
613	76.5	6.4	415	2	Q5UES7	ECOLI	Q5ues7	686	76	6.4	1046	2	Q7PVU9	ANOGA	Q7pvu9	anopheles g
614	76.5	6.4	415	2	Q7UB13	SHIFL	Q7ub13	687	76	6.4	1297	2	Q3XSP4	9PROT	Q3xsp4	magnetococc
615	76.5	6.4	415	2	Q83PL5	SHIFL	Q83pl5	688	76	6.4	1301	1	DXH9	CABEL	Q22307	caenorhabdi

689	1409	2	Q4DUZ9 TRYCR	Q4duz9	trypanosoma	762	75.5	6.3	491	2	Q6SWJ1_HCMV	Q6swj1	human cytom
690	1480	1	CFTR_RABIT	Q00554	oryctolagus	763	75.5	6.3	491	2	Q6SW2_HCMV	Q6sw2	human cytom
691	1551	1	Q6WN4 VENIN	Q06W4	venturia in	764	75.5	6.3	491	2	Q6SWY2_HCMV	Q6swy2	human cytom
692	1783	2	Q18698 CAEEL	Q18698	caenorhabdi	765	75.5	6.3	491	2	Q6SWY1_HCMV	Q6swy1	human cytom
693	1877	2	Q8MQAL CAEEL	Q8mqal	caenorhabdi	766	75.5	6.3	498	2	Q47543_CHLEU	Q47543	chlamydomon
694	2009	2	Q7RBP2 PLAYO	Q7rbp2	plasmodium	767	75.5	6.3	501	2	Q6CHZ5_YARLI	Q6chz5	yarrowia li
695	3010	2	P90191_9HEPC	P90191	hepatitis c	768	75.5	6.3	521	2	Q40JQ8_EHRCH	Q40jq8	ehrlichia c
696	3010	2	P90193_9HEPC	P90193	hepatitis c	769	75.5	6.3	539	2	Q5C152_CRYHO	Q5c152	cryptospori
697	3010	2	P90194_9HEPC	P90194	hepatitis c	770	75.5	6.3	551	1	FLVC2_MOUSE	Q91x85	mus musculus
698	3156	1	MTR1A_RAT	P49218	rattus norv	771	75.5	6.3	574	2	Q22917_SHEWANA	Q22917	shewanella
699	3162	2	Q66PG7_XENIA	Q66pg7	xenopus lae	772	75.5	6.3	574	2	Q36GT8_9GNMM	Q36gt8	shewanella
700	3203	2	Q2XP33_BACSU	Q2xp33	bacillus su	773	75.5	6.3	593	2	Q25322_HELPY	Q25322	helicobacte
701	3206	2	Q61TR8_CAEER	Q61tr8	caenorhabdi	774	75.5	6.3	646	2	Q5ZLM5_CHICK	Q5zlm5	gallus gall
702	3220	2	Q633A3_BACCZ	Q633a3	bacillus ce	775	75.5	6.3	708	2	Q22806_CAEEL	Q22806	caenorhabdi
703	3228	2	Q9VUN8_DROME	Q9vun8	drosophila	776	75.5	6.3	746	2	Q8PCM4_XANAC	Q8pcm4	xanthomonas
704	3231	2	Q6MD11_PARUM	Q6md11	parachlamyd	777	75.5	6.3	773	2	Q96325_ARATH	Q96325	arabidopsis
705	3244	2	Q6B927_RATIL	Q6b927	gracilaria	778	75.5	6.3	775	1	CLCA_ARATH	P92941	arabidopsis
706	3247	2	Q7TP13_RAT	Q7tp13	rattus norv	779	75.5	6.3	795	2	Q61F16_CAEER	Q61f16	caenorhabdi
707	3248	2	Q63E29_BACCZ	Q63ez9	bacillus ce	780	75.5	6.3	939	2	Q5EG34_EMENI	Q5eg34	aspergillus c
708	3248	2	Q6HMF5_BACCH	Q6hmf5	bacillus th	781	75.5	6.3	1008	2	Q89154_9HEPC	Q89154	hepatitis c
709	3263	2	Q63GB2_BACCZ	Q63gb2	bacillus ce	782	75.5	6.3	1010	2	Q3HAL4_TRIER	Q3hal4	trichodesmi
710	3263	2	Q6HNS6_BACHK	Q6hns6	bacillus th	783	75.5	6.3	1088	2	Q4UI92_THEAN	Q4ui92	theileria a
711	3263	2	Q81YU8_BACAN	Q81yu8	bacillus an	784	75.5	6.3	1142	2	Q9UT41_SCHPO	Q9ut41	schizosacch
712	3263	2	Q8CYF4_STRR6	Q8cyf4	streptococc	785	75.5	6.3	1583	2	Q7P9S4_RICSI	Q7p9s4	rickettsia
713	3263	2	Q97PD2_STRPN	Q97pd2	streptococc	786	75.5	6.3	3010	2	Q9J3G7_9HEPC	Q9j3g7	hepatitis c
714	3266	2	Q51PF7_XENIA	Q51pf7	perognathus	787	75	6.3	105	2	Q5AM04_CANAL	Q5am04	candida alb
715	3266	2	Q66PG6_XENIA	Q66pg6	xenopus lae	788	75	6.3	132	2	Q6N505_RHOPA	Q6n505	rhodopseudo
716	3278	2	Q86SK7_MACEU	Q86sk7	macropus eu	789	75	6.3	152	2	Q2N8U7_9SPHN	Q2n8u7	erythrobact
717	3279	2	Q3BSJ4_XANC5	Q3bsj4	xanthomonas	790	75	6.3	156	2	Q81498_9HEPC	Q81498	hepatitis c
718	3282	2	Q3A9G4_CARHZ	Q3a9g4	carboxydoth	791	75	6.3	152	2	Q81507_9HEPC	Q81507	hepatitis c
719	3303	2	Q9KZ08_STRCO	Q9kz08	streptomyce	792	75	6.3	156	2	Q81531_9HEPC	Q81531	hepatitis c
720	3305	2	Q4S7P1_TETNG	Q4s7p1	tetraodon n	793	75	6.3	170	2	Q4Y7N2_PLACH	Q4y7n2	plasmodium
721	3309	2	Q5C281_SCHUA	Q5c281	schistosoma	794	75	6.3	194	2	Q3J4F0_RHOSA	Q3j4f0	rhodobacter
722	3326	2	Q9ESJ3_RAT	Q9esj3	rattus norv	795	75	6.3	202	2	Q36M19_MABHY	Q36m19	marinobacte
723	3339	2	Q9KSB3_VIBCH	Q9ksb3	vibrio chol	796	75	6.3	215	2	Q34238_CAFSU	Q34238	capricornis
724	3342	2	Q59TA5_CANAL	Q59ta5	candida alb	797	75	6.3	215	2	Q336X2_ARYSA	Q336x2	oryza sativ
725	3342	2	Q90EV3_HVH8	Q90ev3	human herpe	798	75	6.3	218	2	Q6SKB1_ORTAU	Q6skb1	arthrobacte
726	3352	1	RNPD_ECO57	P58325	escherichia	799	75	6.3	220	2	Q4L9S9_STAHH	Q4l9s9	staphylococ
727	3352	1	RNPD_ECOLI	P76182	escherichia	800	75	6.3	220	2	Q5FF13_EHRRG	Q5ff13	ehrlichia r
728	3352	2	Q320Y7_SHIBS	Q320y7	shigella bo	801	75	6.3	225	2	Q6VMD0_9CORA	Q6vmd0	infectious
729	3352	2	Q32FE3_SHIDS	Q32fe3	shigella dy	802	75	6.3	227	2	Q9GAT3_OCHHY	Q9gat3	ochotona hy
730	3352	2	Q321Y5_SHISS	Q32ly5	shigella so	803	75	6.3	227	2	Q3RXW8_RALME	Q3rxw8	ralstonia m
731	3352	2	Q2MB69_ECOLI	Q2mb69	escherichia	804	75	6.3	228	2	Q4YQG6_PLABE	Q4yqg6	plasmodium
732	3352	2	Q8FH94_ECOL6	Q8fh94	escherichia	805	75	6.3	232	2	Q3CFK0_THEET	Q3cfk0	thermoanaer
733	3352	2	Q83KY5_SHIFL	Q83ky5	shigella fl	806	75	6.3	249	1	Y1368_METJA	Q58763	methanococc
734	3364	2	Q2ULL9_ASPOR	Q2ul9	aspergillus	807	75	6.3	256	2	Q631U3_BACCZ	Q631u3	bacillus ce
735	3369	2	Q3C185_THBET	Q3c185	thermoanaer	808	75	6.3	273	2	Q3VLP9_9CHLB	Q3vlp9	pelodictyon
736	3371	2	Q2USP9_ASPOR	Q2usp9	aspergillus	809	75	6.3	273	2	Q9KND0_VIBCH	Q9knd0	vibrio chol
737	3377	2	Q4R2L1_VABRI	Q4r2l1	vargula hil	810	75	6.3	277	2	Q6MNA3_BDEBA	Q6mna3	bdellovibri
738	3379	1	CYB_ZAPTR	Q9xnn1	zapus trino	811	75	6.3	280	2	Q44K03_CHRSL	Q44k03	chromohalob
739	3379	2	Q50EJ8_PERFA	Q50ej8	perognathus	812	75	6.3	294	2	Q8RET4_FUSNN	Q8ret4	fusobacteri
740	3389	2	Q8AYS5_HYLJA	Q8ays5	hyla japoni	813	75	6.3	302	2	Q6CVK2_KLULA	Q6cvk2	kluyveromyc
741	3397	2	Q9N4R5_CAEEL	Q9nr45	caenorhabdi	814	75	6.3	311	2	Q5ZLGC_CHICK	Q5zlgc	gallus gall
742	3397	2	Q6RXC2_HCMV	Q6rxc2	human cytom	815	75	6.3	318	2	Q4SMC3_TETNG	Q4smc3	tetraodon n
743	3400	2	Q421Y5_PLABE	Q42ly5	plasmodium	816	75	6.3	330	2	Q58239_PYRHO	Q58239	pyrococcus
744	3401	2	Q3SSF2_NITWN	Q3ssf2	nitrobacter	817	75	6.3	368	2	Q467V3_METBA	Q467v3	methanosarc
745	3410	2	Q70NW4_9BILA	Q70nw4	strongyloid	818	75	6.3	371	2	Q3TS71_MOUSE	Q3ts71	mus musculu
746	3413	2	Q5UET7_ECOLI	Q5uet7	escherichia	819	75	6.3	371	2	Q8BW45_MOUSE	Q8bw45	m 2 days pr
747	3415	1	TNAB_ECO57	Q2NAB	escherichia	820	75	6.3	373	1	PE2R3_PIG	P50131	sus scrofa
748	3415	1	TNAB_ECOLI	Q5UEU4	escherichia	821	75	6.3	375	2	Q4BME7_PSE14	Q4bme7	pseudomonas
749	3415	2	Q31UM3_SHIBS	Q31um3	shigella bo	822	75	6.3	380	1	CYB_RANRU	Q9t6r3	rana rugosa
750	3415	2	Q31UM3_SHIBS	Q31um3	shigella bo	823	75	6.3	380	2	Q69GJ2_9PERO	Q69gj2	nandus nebu
751	3415	2	Q8FVU1_ECOL6	Q8fvu1	escherichia	824	75	6.3	387	2	Q46657_PIG	Q46657	sus scrofa
752	3417	2	Q2VTE8_APLICA	Q2vte8	aplysia cal	825	75	6.3	407	2	Q7NRF5_CHRVO	Q7nrf5	chromobacte
753	3421	2	Q2P2G3_XANOR	Q2p2g3	xanthomonas	826	75	6.3	418	2	Q6QFB8_LEGPN	Q6qfb8	legionella
754	3430	2	Q5X337_LEGPA	Q5x337	legionella	827	75	6.3	418	2	Q6A8T1_PROAC	Q6a8t1	propionibac
755	3433	2	Q6F3C9_CAEEL	Q6f3c9	caenorhabdi	828	75	6.3	418	2	Q5WZ83_LEGPL	Q5wz83	legionella
756	3446	2	Q7S8U0_NEUCR	Q7s8u0	neurospora	829	75	6.3	418	2	Q5X7T2_LEGPA	Q5x7t2	legionella
757	3466	2	Q4I729_PLACH	Q4i729	plasmodium	830	75	6.3	424	2	Q2N984_9SPHN	Q2n984	erythrobact
758	3471	1	5HT2A_MOUSE	P35363	mus musculus	831	75	6.3	425	2	Q427S9_PLABE	Q427s9	plasmodium
759	3471	2	Q543D4_MOUSE	Q543d4	mus musculus	832	75	6.3	460	2	Q2S7B9_BURTH	Q2s7b9	burkholderi
760	3481	2	Q8COK0_MOUSE	Q8cok0	mus musculus	833	75	6.3	460	2	Q3JN15_BURP1	Q3jnl5	burkholderi
761	3482	2	Q9P6J0_SCHPO	Q9p6j0	schizosacch	834	75	6.3	460	2	Q62GF6_BURMA	Q62gf6	burkholderi

835	75	6.3	460	2	Q63QA3_BURPS	Q63qa3_burkholderi	908	74.5	6.2	377	2	Q4R254_VARHI	Q4r254_vargula_hil
836	75	6.3	473	1	GBRRI_HUMAN	P24046_homo_sapien	909	74.5	6.2	377	2	Q4R268_VARHI	Q4r268_vargula_hil
837	75	6.3	473	2	Q9BX06_HUMAN	Q9bx06_homo_sapien	910	74.5	6.2	377	2	Q4R273_VARHI	Q4r273_vargula_hil
838	75	6.3	476	2	Q46N18_RALEJ	Q46n18_ralstonia_e	911	74.5	6.2	377	2	Q4R285_VARHI	Q4r285_vargula_hil
839	75	6.3	488	2	Q7RW58_NEUCR	Q7rw58_neurospora	912	74.5	6.2	377	2	Q4R286_VARHI	Q4r286_vargula_hil
840	75	6.3	498	2	Q7SU67_FUGRU	Q7su67_fugu_rubrip	913	74.5	6.2	377	2	Q4R288_VARHI	Q4r288_vargula_hil
841	75	6.3	526	2	Q9SN21_ARATH	Q9sn21_arabidopsis	914	74.5	6.2	377	2	Q4R289_VARHI	Q4r289_vargula_hil
842	75	6.3	543	2	Q7NS50_CHRVO	Q7ns50_chromobacte	915	74.5	6.2	377	2	Q4R290_VARHI	Q4r290_vargula_hil
843	75	6.3	625	1	KUP2_LEGPH	Q5zt95_legionella	916	74.5	6.2	377	2	Q4R292_VARHI	Q4r292_vargula_hil
844	75	6.3	649	2	Q34952_BACSU	Q34952_bacillus_su	917	74.5	6.2	377	2	Q4R294_VARHI	Q4r294_vargula_hil
845	75	6.3	662	2	Q7VED4_PROMA	Q7ved4_prochloroco	918	74.5	6.2	377	2	Q4R295_VARHI	Q4r295_vargula_hil
846	75	6.3	753	2	Q98S90_GUITH	Q98s90_guillardia	919	74.5	6.2	377	2	Q4R296_VARHI	Q4r296_vargula_hil
847	75	6.3	761	2	Q3GE97_9FIRM	Q3ge97_syntrophomo	920	74.5	6.2	377	2	Q4R299_VARHI	Q4r299_vargula_hil
848	75	6.3	777	2	Q6BG55_PARTE	Q6bg55_parmecium	921	74.5	6.2	377	2	Q4R2A2_VARHI	Q4r2a2_vargula_hil
849	75	6.3	834	2	Q2I6B0_RAT	Q2i6b0_rattus_norv	922	74.5	6.2	377	2	Q4R2A9_VARHI	Q4r2a9_vargula_hil
850	75	6.3	838	2	Q4HZA9_GIBZE	Q4hza9_gibberella	923	74.5	6.2	377	2	Q4R2B4_VARHI	Q4r2b4_vargula_hil
851	75	6.3	883	2	Q4N412_THEPA	Q4n412_thelateria_p	924	74.5	6.2	377	2	Q4R2C4_VARHI	Q4r2c4_vargula_hil
852	75	6.3	885	2	Q8PU16_METMA	Q8pu16_methanobarc	925	74.5	6.2	377	2	Q4R2C9_VARHI	Q4r2c9_vargula_hil
853	75	6.3	937	2	Q82ZR7_ENTFA	Q82zr7_enterococcu	926	74.5	6.2	377	2	Q4R2D6_VARHI	Q4r2d6_vargula_hil
854	75	6.3	1008	2	Q89152_9HEPC	Q89152_hepatitis_c	927	74.5	6.2	377	2	Q4R2E3_VARHI	Q4r2e3_vargula_hil
855	75	6.3	1008	2	Q89153_9HEPC	Q89153_hepatitis_c	928	74.5	6.2	377	2	Q4R2E4_VARHI	Q4r2e4_vargula_hil
856	75	6.3	1008	2	Q89156_9HEPC	Q89156_hepatitis_c	929	74.5	6.2	377	2	Q4R2E7_VARHI	Q4r2e7_vargula_hil
857	75	6.3	1131	2	Q8NAT5_HUMAN	Q8nat5_homo_sapien	930	74.5	6.2	377	2	Q4R2F7_VARHI	Q4r2f7_vargula_hil
858	75	6.3	1145	2	Q8GUE7_9LILI	Q8gue7_cymodocea_n	931	74.5	6.2	377	2	Q4R2G0_VARHI	Q4r2g0_vargula_hil
859	75	6.3	1146	2	Q3ILG0_PSEHT	Q3ilg0_pseudoalter	932	74.5	6.2	377	2	Q4R2H6_VARHI	Q4r2h6_vargula_hil
860	75	6.3	1154	2	Q6FTI6_CANGA	Q6fti6_candida_gla	933	74.5	6.2	377	2	Q4R2H9_VARHI	Q4r2h9_vargula_hil
861	75	6.3	1336	2	Q6FLJ1_MESFL	Q6flj1_mesoplasma	934	74.5	6.2	377	2	Q4R2H9_VARHI	Q4r2h9_vargula_hil
862	75	6.3	1703	2	Q38B01_9TRYP	Q38b01_trypanosoma	935	74.5	6.2	377	2	Q4R2I1_VARHI	Q4r2i1_vargula_hil
863	75	6.3	1704	2	Q95Z06_9TRYP	Q95z06_trypanosoma	936	74.5	6.2	377	2	Q4R2J3_VARHI	Q4r2j3_vargula_hil
864	75	6.3	2248	1	CYAI_DROME	P32870_drosophila	937	74.5	6.2	377	2	Q4R2K1_VARHI	Q4r2k1_vargula_hil
865	75	6.3	2846	2	Q55EL4_DICDI	Q55el4_dictyosteli	938	74.5	6.2	377	2	Q4R2K2_VARHI	Q4r2k2_vargula_hil
866	75	6.3	3010	2	Q68833_9HEPC	Q68833_hepatitis_c	939	74.5	6.2	377	2	Q4R2K3_VARHI	Q4r2k3_vargula_hil
867	75	6.3	3010	2	Q9J3G2_9HEPC	Q9j3g2_hepatitis_c	940	74.5	6.2	377	2	Q4R2K5_VARHI	Q4r2k5_vargula_hil
868	75	6.3	3010	2	Q9J3G5_9HEPC	Q9j3g5_hepatitis_c	941	74.5	6.2	377	2	Q4R2K8_VARHI	Q4r2k8_vargula_hil
869	75	6.3	3010	2	Q9QIY7_9HEPC	Q9qi7_hepatitis_c	942	74.5	6.2	377	2	Q4R2M1_VARHI	Q4r2m1_vargula_hil
870	75	6.3	3010	2	Q9QIY8_9HEPC	Q9qi8_hepatitis_c	943	74.5	6.2	377	2	Q4R2M8_VARHI	Q4r2m8_vargula_hil
871	74.5	6.2	159	2	Q34A83_RHOPA	Q34a83_rhodopseudo	944	74.5	6.2	377	2	Q4R2M9_VARHI	Q4r2m9_vargula_hil
872	74.5	6.2	174	2	P97068_9ENTR	P97068_salmonella	945	74.5	6.2	377	2	Q4R2N2_VARHI	Q4r2n2_vargula_hil
873	74.5	6.2	179	2	Q8EPH9_OCEIH	Q8eph9_oceanobacil	946	74.5	6.2	377	2	Q4R2N4_VARHI	Q4r2n4_vargula_hil
874	74.5	6.2	180	2	P71253_ECOLI	P71253_escherichia	947	74.5	6.2	377	2	Q4R2N5_VARHI	Q4r2n5_vargula_hil
875	74.5	6.2	222	2	Q32DT0_SHIDS	Q32dt0_shigella_dy	948	74.5	6.2	377	2	Q4R2N6_VARHI	Q4r2n6_vargula_hil
876	74.5	6.2	227	2	Q9GAT4_OCHCU	Q9gat4_ochotona_cu	949	74.5	6.2	377	2	Q4R2P2_VARHI	Q4r2p2_vargula_hil
877	74.5	6.2	227	2	Q9GAT5_OCHTI	Q9gat5_ochotona_th	950	74.5	6.2	377	2	Q666W3_VARHI	Q66w3_vargula_hil
878	74.5	6.2	227	2	Q9GAT6_OCHTR	Q9gat6_ochotona_tr	951	74.5	6.2	378	2	Q6DUV8_BRANA	Q6duv8_brassica_na
879	74.5	6.2	258	2	Q88WC7_LACPL	Q88wc7_lactobacill	952	74.5	6.2	379	1	CYB_OCHPR	Q6duv8_ochotona_pr
880	74.5	6.2	278	2	Q9R905_RHIME	Q9r905_rhizobium_m	953	74.5	6.2	379	2	Q6ELW8_OCHPR	Q6elw8_ochotona_pr
881	74.5	6.2	278	2	Q2RIL5_ORYSA	Q2ril5_oryza_sativ	954	74.5	6.2	379	2	Q8BEW5_APLRU	Q8bew5_aplodontia
882	74.5	6.2	280	2	Q6WIF6_SYNFP	Q6wif6_synecococc	955	74.5	6.2	379	2	Q9B9E3_CHAPN	Q9b9e3_chaetodipus
883	74.5	6.2	290	2	Q6SEU1_9BACT	Q6seu1_uncultured	956	74.5	6.2	392	2	Q9LCN4_MICOL	Q9lcn4_micromonospor
884	74.5	6.2	294	2	Q4CJ11_CLOTM	Q4cj11_clostridium	957	74.5	6.2	415	2	Q4A6X7_MYCS5	Q4a6x7_mycoplasma
885	74.5	6.2	298	2	Q5LEN3_ENTHI	Q5len3_debaryomyce	958	74.5	6.2	442	2	Q94A13_ARATH	Q94a13_arabidopsis
886	74.5	6.2	298	2	Q6BWD3_DEBHA	Q6bwd3_entamoeba_h	959	74.5	6.2	450	1	ALG10_CANAL	Q59yv2_candida_alb
887	74.5	6.2	313	2	Q8R7K6_THETA	Q8r7k6_thermoanaer	960	74.5	6.2	458	2	Q65MD8_BACLD	Q65md8_bacillus_li
888	74.5	6.2	335	2	Q9WXS7_THEMA	Q9wxs7_thermotoga	961	74.5	6.2	471	1	5HT2A_RAT	P14842_rattus_norv
889	74.5	6.2	346	2	CX3C1_HUMAN	P49238_homo_sapien	962	74.5	6.2	471	2	Q4U3W9_MESAU	Q4u3w9_mesocricetu
890	74.5	6.2	355	1	Q5WHM9_BACSK	Q5whm9_bacillus_cl	963	74.5	6.2	473	2	Q9K5Y9_BACHID	Q9k5y9_bacillus_ha
891	74.5	6.2	358	2	Q48VO7_STREM	Q48vo7_streptococc	964	74.5	6.2	488	2	Q6QU71_ASPUT	Q6qu71_aspergillus
892	74.5	6.2	363	2	Q8IDY2_PLAF7	Q8idy2_plasmodium	965	74.5	6.2	500	2	Q24348_SORBI	Q24348_sorghum_bic
893	74.5	6.2	364	2	Q4R1V2_VARHI	Q4r1v2_vargula_hil	966	74.5	6.2	510	2	Q2RU28_RHORI	Q2ru28_rhodospiril
894	74.5	6.2	377	2	Q4R1V3_VARHI	Q4r1v3_vargula_hil	967	74.5	6.2	523	2	Q55UE4_CRYNE	Q55ue4_cryptococcu
895	74.5	6.2	377	2	Q4R1V6_VARHI	Q4r1v6_vargula_hil	968	74.5	6.2	523	2	Q5K102_CRYNE	Q5k102_cryptococcu
896	74.5	6.2	377	2	Q4R1W3_VARHI	Q4r1w3_vargula_hil	969	74.5	6.2	540	2	Q66GQ5_ARATH	Q66gq5_arabidopsis
897	74.5	6.2	377	2	Q4R1X3_VARHI	Q4r1x3_vargula_hil	970	74.5	6.2	562	2	Q8N2S3_HUMAN	Q8n2s3_homo_sapien
898	74.5	6.2	377	2	Q4R1Y1_VARHI	Q4r1y1_vargula_hil	971	74.5	6.2	574	2	O22454_WHEAT	O22454_triticum_ae
899	74.5	6.2	377	2	Q4R1Y8_VARHI	Q4r1y8_vargula_hil	972	74.5	6.2	594	2	Q4WLQ1_ASPPT	Q4wlq1_aspergillus
900	74.5	6.2	377	2	Q4R1Z4_VARHI	Q4r1z4_vargula_hil	973	74.5	6.2	597	2	Q9VD40_DROME	Q9vd40_drosophila
901	74.5	6.2	377	2	Q4R1Z6_VARHI	Q4r1z6_vargula_hil	974	74.5	6.2	615	2	Q3IEZ1_PSSHT	Q3iez1_pseudoalter
902	74.5	6.2	377	2	Q4R1Z8_VARHI	Q4r1z8_vargula_hil	975	74.5	6.2	618	1	YKR4_YEAST	P36029_saccharomyc
903	74.5	6.2	377	2	Q4R201_VARHI	Q4r201_vargula_hil	976	74.5	6.2	620	2	Q2X3C4_9GAMM	Q2x3c4_shewanella
904	74.5	6.2	377	2	Q4R222_VARHI	Q4r222_vargula_hil	977	74.5	6.2	620	2	Q2ZVR1_SHEPU	Q2zvr1_shewanella
905	74.5	6.2	377	2	Q4R223_VARHI	Q4r223_vargula_hil	978	74.5	6.2	620	2	Q361N8_9GAMM	Q361n8_shewanella
906	74.5	6.2	377	2	Q4R244_VARHI	Q4r244_vargula_hil	979	74.5	6.2	793	2	Q4PCY9_USTMA	Q4pcy9_ustilago_ma
907	74.5	6.2	377	2			980	74.5	6.2	848	2	Q8VVK9_CORGL	Q8vvk9_corynebacte

981	74.5	1	FTSK_VIBVU	990	6.2	990	Q8d8m2 vibrio vuln	1054	74	6.2	396	2	Q7A6D3_STAAN	Q7a6d3 staphylococ
982	74.5	2	Q3H520_9ACTO	1004	6.2	1004	Q3h520 nocardioide	1055	74	6.2	396	2	Q8NXC4_STAAM	Q8nxc4 staphylococ
983	74.5	2	Q4UBN7_THEAN	1022	6.2	1022	Q4ubn7 theilleria a	1056	74	6.2	396	2	Q9YV76_STAAM	Q9yv76 staphylococ
984	74.5	2	Q38FL3_9TRYP	1023	6.2	1023	Q38fl3 trypanosoma	1057	74	6.2	396	2	Q5HH70_STAAC	Q5hh70 staphylococ
985	74.5	2	Q382A3_9TRYP	1033	6.2	1033	Q382a3 trypanosoma	1058	74	6.2	397	2	Q4Z254_PLABE	Q4z254 plasmodium
986	74.5	2	Q722C1_TRYBB	1033	6.2	1033	Q722c1 trypanosoma	1059	74	6.2	398	2	Q2PQV8_NOCA	Q2pqv8 rhodococcus
987	74.5	2	Q722C0_9TRYP	1034	6.2	1034	Q722c0 trypanosoma	1060	74	6.2	398	2	Q5NEU8_PRAFT	Q5neu8 francisella
988	74.5	2	Q94447_CALIPH	1061	6.2	1061	Q94447 caliphora	1061	74	6.2	406	2	Q3FF83_9BURK	Q3ff83 burkholderi
989	74.5	2	Q61PW5_CAEER	1183	6.2	1183	Q61pw5 caenorhabdi	1062	74	6.2	410	2	Q4R103_TETNG	Q4ri03 tetraodon n
990	74.5	2	Q8T687_DICDI	1520	6.2	1520	Q8t687 dictyosteli	1063	74	6.2	418	2	Q6QF89_LEGPN	Q6qfb9 legioneella
991	74.5	2	Q54TV1_DICDI	1534	6.2	1534	Q54tv1 dictyosteli	1064	74	6.2	418	2	Q6QFC5_LEGPN	Q6qfc5 legioneella
992	74.5	2	Q780S1_NEUCR	1559	6.2	1559	Q780s1 neurospora	1065	74	6.2	418	2	Q6QFC7_LEGPN	Q6qfc7 legioneella
993	74.5	2	Q54Z25_DICDI	1640	6.2	1640	Q54z25 dictyosteli	1066	74	6.2	436	2	Q5QZG8_IDILO	Q5qzg8 idiomarina
994	74.5	2	Q9LYS6_ARATH	1808	6.2	1808	Q9lys6 arabidopsis	1067	74	6.2	442	2	Q9CEG6_LACIA	Q9ceg6 lactococcus
995	74.5	2	Q8IKF1_PLAPF	1837	6.2	1837	Q8ikf1 plasmodium	1068	74	6.2	452	2	Q2Z5B2_9GAMM	Q2z5b2 shewanella
996	74.5	2	Q91AU0_9HEPC	3010	6.2	3010	Q91au0 hepatitis c	1069	74	6.2	452	2	Q4NJCT_9MICC	Q4njct arthrobacte
997	74	2	Q8K426_CHLTE	124	6.2	124	Q8k426 chlorobium	1070	74	6.2	457	2	Q8RBZ7_THETN	Q8rbz7 thermoanaer
998	74	2	Q81528_9HEPC	156	6.2	156	Q81528 hepatitis c	1071	74	6.2	459	2	Q39U36_GEOMG	Q39u36 geobacter m
999	74	2	Q8WZ72_HUMAN	167	6.2	167	Q8wz72 homo sapien	1072	74	6.2	475	2	Q9S2G7_STRCO	Q9s2g7 streptomyce
1000	74	2	Q5VHX0_EAV	173	6.2	173	Q5vnx0 equine arte	1073	74	6.2	481	2	Q4Q1F4_LHIMA	Q4q1f4 leishmania
1001	74	2	Q3ZSX9_PLAVI	193	6.2	193	Q3zsx9 plasmodium	1074	74	6.2	485	2	Q9XVKO_CABEL	Q9xvko caenorhabdi
1002	74	2	Q5HCD2_EHRRW	220	6.2	220	Q5hcd2 ehrlichia r	1075	74	6.2	487	2	Q23384_ARATH	Q23384 arabidopsis
1003	74	2	Q91SA2_9CORO	225	6.2	225	Q91sa2 infectious	1076	74	6.2	493	2	Q9EVJ7_FLALU	Q9evj7 flavobacter
1004	74	2	Q88V70_LACPL	230	6.2	230	Q88v70 lactobacill	1077	74	6.2	503	2	Q6M052_METMP	Q6m052 methanococc
1005	74	2	1_C0BS2_ARCFU	231	6.2	231	027961 archaeoglob	1078	74	6.2	505	2	Q21KZ1_9DELT	Q21kz1 anaeromyxob
1006	74	2	Q28892_ARCFU	231	6.2	231	028892 archaeoglob	1079	74	6.2	528	2	Q701Q9_KJULA	Q701q9 kluyveromyc
1007	74	2	Q6HET1_BACHK	238	6.2	238	Q6het1 bacillus th	1080	74	6.2	530	2	Q41SG0_FERAC	Q41sg0 ferroplasma
1008	74	2	Q366H4_9GAMM	249	6.2	249	Q366h4 shewanella	1081	74	6.2	530	2	Q51FL8_ENTHI	Q51fl8 entamoeba h
1009	74	2	Q66483_EAV	255	6.2	255	Q66483 equine arte	1082	74	6.2	540	2	Q61F33_PLAF7	Q61f33 plasmodium
1010	74	2	Q31RM0_SYNP7	262	6.2	262	Q31rw0 synecococc	1083	74	6.2	581	2	Q6F1I6_CANGA	Q6f1i6 candida gla
1011	74	2	Q6CUI8_KJULA	278	6.2	278	Q6cui8 kluyveromyc	1084	74	6.2	584	2	Q5KA08_CRYNE	Q5ka08 cryptococcu
1012	74	2	Q4XPR5_PLACD	279	6.2	279	Q4xpr5 plasmodium	1085	74	6.2	587	2	Q43QW4_SOLUS	Q43qw4 solibacter
1013	74	2	Q4E472_TRYCR	285	6.2	285	Q4e472 trypanosoma	1086	74	6.2	599	2	Q5KA09_CRYNE	Q5ka09 cryptococcu
1014	74	2	POTB_MYCPN	286	6.2	286	P75058 mycoplasma	1087	74	6.2	650	2	Q9S6S6_9ACT	Q9s6s6 lactococcus
1015	74	2	Q4AVT5_9BURK	291	6.2	291	Q4avt5 polaromonas	1088	74	6.2	681	2	Q4FTS7_PSYAR	Q4fts7 psychrobact
1016	74	2	Q6G9G8_YERPS	291	6.2	291	Q6g9g8 versinia ps	1089	74	6.2	689	2	Q37RQ8_SPHAR	Q37rq8 novosphingo
1017	74	2	1_CYOB_PSEPU	295	6.2	295	Q694m3 pseudomonas	1090	74	6.2	742	2	Q6FNV6_CANGA	Q6fnv6 candida gla
1018	74	2	Q6S4M3_PSEPU	295	6.2	295	Q6s4m3 pseudomonas	1091	74	6.2	841	2	Q9A1P1_CARRU	Q9a1p1 carsonella
1019	74	2	Q416Y2_KINRA	295	6.2	295	Q416y2 kinococcus	1092	74	6.2	846	2	Q9JU47_CARRU	Q9ju47 carsonella
1020	74	2	Q61BC3_CAEER	297	6.2	297	Q61bc3 caenorhabdi	1093	74	6.2	892	2	Q8TGB2_CANAL	Q8tgb2 candida alb
1021	74	2	NU2M_ASCSU	300	6.2	300	P24877 ascaris suu	1094	74	6.2	943	2	Q41M19_GIBZE	Q41m19 gibberella
1022	74	2	Q3DP19_STRAG	309	6.2	309	Q3dp19 streptococ	1095	74	6.2	1123	2	Q9SE99_ARATH	Q9se99 arabidopsis
1023	74	2	1_PYRB_AERPE	312	6.2	312	Q9ybd4 aeropyrum p	1096	74	6.2	1216	2	Q9SPU7_ARATH	Q9spu7 arabidopsis
1024	74	2	Q9CH74_LACLA	312	6.2	312	Q9ch74 lactococcus	1097	74	6.2	1216	2	Q5S1S2_CRYNE	Q5s1s2 cryptococcu
1025	74	2	Q710S2_SPAEH	315	6.2	315	Q710s2 spalax leuc	1098	74	6.2	1216	2	Q8KXZ1_CRYNE	Q8kxz1 cryptococcu
1026	74	2	Q8M6V0_9MAXI	321	6.2	321	Q8m6v0 tigreptococ	1099	74	6.2	3010	2	Q913V3_9HEPC	Q913v3 hepatitis c
1027	74	2	Q8DVZ6_STRMU	321	6.2	321	Q8dvz6 streptococ	1100	74	6.2	3010	2	Q9DTE8_9HEPC	Q9dte8 hepatitis c
1028	74	2	Q3TU35_MOUSE	334	6.2	334	Q3tu35 mus musculu	1101	74	6.2	3010	2	Q9J3H6_9HEPC	Q9j3h6 hepatitis c
1029	74	2	Q3H0J8_9ACTO	331	6.2	331	Q3h0j8 nocardioide	1102	74	6.2	3010	2	Q9Q1Y1_9HEPC	Q9q1y1 hepatitis c
1030	74	2	Q4FNS1_PELUB	333	6.2	333	Q4fns1 pelagibacte	1103	74	6.2	3010	2	Q9Q1Y2_9HEPC	Q9q1y2 hepatitis c
1031	74	2	Q621V1_CAEER	339	6.2	339	Q621v1 caenorhabdi	1104	73.5	6.2	120	2	Q9SKA6_ARATH	Q9ska6 arabidopsis
1032	74	2	Q621V1_CAEER	342	6.2	342	Q621v1 caenorhabdi	1105	73.5	6.2	153	2	Q92XD3_RHIME	Q92xd3 rhizobium m
1033	74	2	1_L10R2_MOUSE	349	6.2	349	Q61190 mus musculu	1106	73.5	6.2	174	2	Q2NGT7_9URY	Q2ngt7 methanosphe
1034	74	2	1_MTRIA_HUMAN	350	6.2	350	P48039 homo sapien	1107	73.5	6.2	180	2	Q8XZS3_PYRAE	Q8xzs3 pyrobaculum
1035	74	2	Q8VHM7_MOUSE	351	6.2	351	Q8vhm7 mus musculu	1108	73.5	6.2	180	2	P71251_ECOLI	P71251 escherichia
1036	74	2	Q65U34_MANSAM	354	6.2	354	Q65u34 mantheimia	1109	73.5	6.2	180	2	P71257_ECOLI	P71257 escherichia
1037	74	2	Q5FV66_MEDTR	357	6.2	357	Q5fv66 medicago tr	1110	73.5	6.2	180	2	P71257_ECOLI	P71257 escherichia
1038	74	2	Q31TR5_NATPD	359	6.2	359	Q31tr5 natronomona	1111	73.5	6.2	199	2	P75018_ECOLI	P75018 escherichia
1039	74	2	Q64AL9_9ARCH	361	6.2	361	Q64al9 uncultured	1112	73.5	6.2	216	1	Y2036_AQUAE	Y2036 aquifex aeo
1040	74	2	Q4CMV5_TRYCR	372	6.2	372	Q4cmv5 trypanosoma	1113	73.5	6.2	217	2	Q4TEY9_TETNG	Q4tey9 tetraodon n
1041	74	2	1_CYB_THOMO	379	6.2	379	Q8wsk2 thomomys mo	1114	73.5	6.2	226	2	Q5MAP0_9CORO	Q5map0 infectious
1042	74	2	Q47980_THOBO	379	6.2	379	Q47980 thomomys bo	1115	73.5	6.2	226	2	Q9T0X1_9CORO	Q9t0x1 infectious
1043	74	2	Q48002_THOMO	379	6.2	379	Q48002 thomomys mo	1116	73.5	6.2	246	2	Q4D4K9_TRYCR	Q4d4k9 trypanosoma
1044	74	2	Q48003_THOMO	379	6.2	379	Q48003 thomomys mo	1117	73.5	6.2	267	2	Q50Z61_ENTHI	Q50z61 entamoeba h
1045	74	2	Q59J17_9SCIU	379	6.2	379	Q59j17 pteromys vo	1118	73.5	6.2	270	2	Q8HBP0_PERLO	Q8hbp0 perognathus
1046	74	2	Q8HJ17_THOBO	379	6.2	379	Q8hj17 thomomys bo	1119	73.5	6.2	270	2	Q8HIY6_PERLO	Q8hiy6 perognathus
1047	74	2	Q8WEK5_THOTA	379	6.2	379	Q8wek5 thomomys ta	1120	73.5	6.2	274	2	Q95L51_CAPHI	Q95l51 capra hircu
1048	74	2	Q74KB0_LACUO	380	6.2	380	Q74kb0 lactobacill	1121	73.5	6.2	278	2	Q4JC08_SULAC	Q4jc08 sulfolobus
1049	74	2	1_CYB_PSENI	381	6.2	381	Q35553 pseudantech	1122	73.5	6.2	281	2	Q3NN12_SHEFR	Q3nn12 shewanella
1050	74	2	Q5R7A1_PONPY	382	6.2	382	Q5r7a1 pongo pygma	1123	73.5	6.2	281	2	Q2SQF4_9GAMM	Q2sqf4 hanelia che
1051	74	2	Q2YWM7_STAAB	396	6.2	396	Q2ywm7 staphylococ	1124	73.5	6.2	286	2	Q4HS16_CAMUP	Q4hsi6 campylobact
1052	74	2	Q6GAR1_STAAS	396	6.2	396	Q6gar1 staphylococ	1125	73.5	6.2	298	2	Q6Z2T3_ORYSA	Q6z2t3 oryza sativ
1053	74	2	Q6G168_STAAR	396	6.2	396	Q6g168 staphylococ	1126	73.5	6.2	303	2	Q5J3K6_RAT	Q5j3k6 rattus norv

1127	73.5	6.2	304	2	Q2RIE6	MOOTH	Q2rie6	moorella th	1200	73.5	6.2	1277	2	Q76G00	CIOIN	Q76g00	ciona intes
1128	73.5	6.2	305	2	Q5NP42	ZYMOG	Q5np42	zymomonas m	1201	73.5	6.2	1287	2	Q7YU59	DROME	Q7yu59	drosephila
1129	73.5	6.2	304	2	Q4POB6	USTWA	Q4pob6	ustilago ma	1202	73.5	6.2	1287	2	Q9U5W1	DROME	Q9u5w1	drosephila
1130	73.5	6.2	306	2	Q37MI0	RHOA	Q37mi0	rhodopsendo	1203	73.5	6.2	1292	2	Q9VL24	DROME	Q9vl24	drosephila
1131	73.5	6.2	307	2	Q2IYAS	RHOA	Q2iyas	rhodopsendo	1204	73.5	6.2	1292	2	Q9AIH0	CARRU	Q9aih0	carsonella
1132	73.5	6.2	316	2	Q3AQX9	CHLCH	Q3aqx9	chlorobium	1205	73.5	6.2	1476	2	Q96SD3	DICDI	Q96sd3	dicyosteli
1133	73.5	6.2	318	2	Q55895	SYNY3	Q55895	synchocyst	1206	73.5	6.2	1545	2	Q8GU65	ORVSA	Q8gu65	oryza sativ
1134	73.5	6.2	338	1	YYAD	BACSU	P37520	bacillus su	1207	73.5	6.2	2666	2	Q6FW99	CANGA	Q6fw99	candida gla
1135	73.5	6.2	355	2	Q4J826	SULAC	Q4j826	sulfolobus	1208	73.5	6.2	3007	2	Q4SR88	TETNG	Q4sr88	tetraodon n
1136	73.5	6.2	359	2	Q2NTQ3	SODGL	Q2ntq3	sodalis glo	1209	73.5	6.2	3010	2	Q9DTE6	9HEPC	Q9dte6	hepatitis c
1137	73.5	6.2	360	2	Q8UW8	BRARE	Q8uw8	brachydanio	1210	73.5	6.2	3381	2	Q8IDK4	PLAF7	Q8idk4	plasmodium
1138	73.5	6.2	367	2	Q64BD6	9ARCH	Q64bd6	uncultured	1211	73.5	6.2	4470	2	Q66WN5	9CORA	Q66wn5	murine hepa
1139	73.5	6.2	373	2	Q5FI17	LACAC	Q5fi17	lactobacill	1212	73.5	6.2	4839	2	Q2N3S8	POICB	Q2n3s8	polyangium
1140	73.5	6.2	379	1	CVB	PHOGR	Q35457	thocma groen	1213	73.5	6.2	7176	1	RIAB	CYMA5	P16342	m replicase
1141	73.5	6.2	379	1	CVB	THOTA	Q48001	thomomys ta	1214	73.5	6.2	7178	2	Q66WN6	9CORA	Q66wn6	murine hepa
1142	73.5	6.2	379	2	Q9G3M8	OCHCU	Q9g3m8	ochotona cu	1215	73	6.1	114	2	Q75XA7	HELPI	Q75xa7	helicobacte
1143	73.5	6.2	379	2	Q508J0	9RODE	Q508j0	perognathus	1216	73	6.1	114	2	Q9ZLU2	HELPI	Q9zlu2	helicobacte
1144	73.5	6.2	379	2	Q508J0	PERPA	Q508j0	perognathus	1217	73	6.1	138	2	Q97777	ELENA	Q97777	elephas max
1145	73.5	6.2	379	2	Q588N8	SCILI	Q588n8	sciurus lis	1218	73	6.1	138	2	Q373Z8	RHOFA	Q373z8	rhodopsendo
1146	73.5	6.2	379	2	Q2N2B6	PERPA	Q2n2b6	perognathus	1219	73	6.1	140	2	Q64145	9MURI	Q64145	rattus sp.
1147	73.5	6.2	380	1	CVB	STRPU	P15547	strongyloce	1220	73	6.1	145	2	Q9UXB0	SULSO	Q9uxb0	sulfolobus
1148	73.5	6.2	384	1	OPGC	SALTI	Q82719	salmonella	1221	73	6.1	155	2	Q7VJPI	HELHP	Q7vjp1	helicobacte
1149	73.5	6.2	384	1	OPGC	SALTY	Q82727	salmonella	1222	73	6.1	156	2	Q81510	9HEPC	Q81510	hepatitis c
1150	73.5	6.2	385	2	P94442	BACSU	P94442	bacillus su	1223	73	6.1	156	2	Q81537	9HEPC	Q81537	hepatitis c
1151	73.5	6.2	387	2	Q9KWU2	9SPHN	Q9kwu2	sphingomona	1224	73	6.1	156	2	Q81537	9HEPC	Q81537	hepatitis c
1152	73.5	6.2	387	2	Q7MVX5	PORGI	Q7mvx5	porphyromon	1225	73	6.1	163	2	Q80RY8	9CORA	Q80ry8	infectious
1153	73.5	6.2	389	1	OXYP	MACMU	P56494	macaca mula	1226	73	6.1	220	2	Q72240	BACCI	Q72240	bacillus ce
1154	73.5	6.2	391	1	OXYP	BOVIN	P56449	bos taurus	1227	73	6.1	223	1	VME1	IBVG	Q910e2	avian infec
1155	73.5	6.2	397	2	Q82ZF7	ENTFA	Q82zf7	enterococcu	1228	73	6.1	223	2	Q91S97	9CORA	Q91s97	infectious
1156	73.5	6.2	398	2	Q3CNW3	ALTAT	Q3cnw3	pseudocalter	1229	73	6.1	226	2	Q779P6	9CORA	Q779p6	infectious
1157	73.5	6.2	409	2	Q7V140	PROMP	Q7v140	prochloroco	1230	73	6.1	238	1	PYRF	BACCR	Q81986	bacillus ce
1158	73.5	6.2	413	2	Q928T3	LISIN	Q928t3	listeria in	1231	73	6.1	238	2	Q4MJ45	BACCE	Q4mj45	bacillus ce
1159	73.5	6.2	421	2	Q8PK37	XANAC	Q8pk37	xanthomonas	1232	73	6.1	238	2	Q636E3	BACCC	Q636e3	bacillus ce
1160	73.5	6.2	425	2	Q6D6K1	ERWCT	Q6d6k1	erwinia car	1233	73	6.1	238	2	Q73216	BACCI	Q73216	bacillus ce
1161	73.5	6.2	435	2	Q48IN0	COLEP3	Q48in0	colwellia p	1234	73	6.1	249	2	Q362R1	9GAMM	Q362r1	shewanella
1162	73.5	6.2	442	2	Q8GZ34	ARATH	Q8gz34	arabidopsis	1235	73	6.1	249	2	Q48TQ7	STRPM	Q48tq7	streptococc
1163	73.5	6.2	442	2	Q9XIQ7	ARATH	Q9xiq7	arabidopsis	1236	73	6.1	249	2	Q7DAL8	STRP1	Q7dal8	streptococc
1164	73.5	6.2	451	2	Q4E247	TRYCR	Q4e247	trypanosoma	1237	73	6.1	249	2	Q9FDU6	STRPY	Q9fdu6	equine arte
1165	73.5	6.2	470	2	Q36Q01	MARHY	Q36q01	marinobacte	1238	73	6.1	255	2	P87639	EAV	P87639	equine arte
1166	73.5	6.2	491	1	VIE1	HCWVA	P13202	human cytom	1239	73	6.1	255	2	Q9YNU0	EAV	Q9ynu0	equine arte
1167	73.5	6.2	491	2	Q6SW28	HCWV	Q6sw28	human cytom	1240	73	6.1	260	2	Q7QN39	ANOAG	Q7qn39	anopheles g
1168	73.5	6.2	518	2	Q7RT44	PLAYO	Q7rt44	plasmodium	1241	73	6.1	264	2	Q7MJ52	VIBVI	Q7mj52	vibrio vuln
1169	73.5	6.2	523	2	Q64WY6	BACFR	Q64wy6	bacteroides	1242	73	6.1	264	2	Q8DAQ9	VIBVI	Q8daq9	vibrio vuln
1170	73.5	6.2	542	2	Q5LG29	BACFN	Q5lg29	bacteroides	1243	73	6.1	265	2	Q36T98	MARHY	Q36t98	marinobacte
1171	73.5	6.2	555	2	Q7PFV1	ANOAG	Q7pfv1	anopheles g	1244	73	6.1	269	2	Q30RA4	THIDN	Q30ra4	thiomicrosp
1172	73.5	6.2	557	2	Q8VZE2	ARATH	Q8vze2	arabidopsis	1245	73	6.1	273	2	Q2K662	RHIET	Q2k662	rhizobium e
1173	73.5	6.2	563	2	Q5ATP6	EMENI	Q5atp6	aspergillus	1246	73	6.1	279	2	Q6TY95	9BILA	Q6ty95	xiphinema a
1174	73.5	6.2	570	2	Q3N230	9DELT	Q3n230	syntrophoba	1247	73	6.1	282	1	NU2M	CAEEL	P24889	caenorhabdi
1175	73.5	6.2	574	2	Q93990	CANAL	Q93990	candida alb	1248	73	6.1	290	2	Q5HG13	STAAC	Q5hg13	staphylococ
1176	73.5	6.2	574	2	Q5A4P9	CANAL	Q5a4p9	candida alb	1249	73	6.1	290	2	Q6G9W4	STAAM	Q6g9w4	staphylococ
1177	73.5	6.2	607	2	Q6DFU5	YENLA	Q6dfu5	xenopus lae	1250	73	6.1	294	2	Q4X7M3	PLACH	Q4x7m3	plasmodium
1178	73.5	6.2	614	2	Q5CE41	CRYHO	Q5ce41	cryptospori	1251	73	6.1	294	2	Q4XT47	PLACH	Q4xt47	plasmodium
1179	73.5	6.2	634	1	KUP	XYLFA	Q3pc78	xylella fas	1252	73	6.1	295	2	Q2XZG6	EMENI	Q2xzg6	aspergillus
1180	73.5	6.2	634	2	Q3R3X0	XYLFA	Q3r3x0	xylella fas	1253	73	6.1	295	2	Q2XDN0	PSEPU	Q2xdn0	pseudomonas
1181	73.5	6.2	634	2	Q3REM6	XYLFA	Q3rem6	xylella fas	1254	73	6.1	295	2	Q8VUO2	PSEPU	Q8vu02	pseudomonas
1182	73.5	6.2	637	1	MUTL	BACHD	Q9kac1	bacillus ha	1255	73	6.1	295	2	Q88PN3	PSEPK	Q88pn3	pseudomonas
1183	73.5	6.2	640	1	APRN	ENTHI	P20301	entamoeba h	1256	73	6.1	303	2	Q94EJ0	ARATH	Q94ej0	arabidopsis
1184	73.5	6.2	641	2	Q3NCP3	9PROT	Q3ncp3	nitrosomona	1257	73	6.1	314	2	Q8ESH3	OCEIH	Q8esh3	oceanobacil
1185	73.5	6.2	653	2	Q8TTH1	METAC	Q8tth1	methanosarc	1258	73	6.1	314	2	Q2K5Y6	RHIET	Q2k5y6	rhizobium e
1186	73.5	6.2	661	2	Q68468	CORAM	Q68468	corynebacte	1259	73	6.1	315	2	Q2KDV3	RHIET	Q2kdv3	rhizobium e
1187	73.5	6.2	715	2	Q5IWR5	GLYGR	Q5iwr5	glyceria gr	1260	73	6.1	319	2	Q2KDV3	RHIET	Q2kdv3	rhizobium e
1188	73.5	6.2	731	2	Q16531	CAEEL	Q16531	caenorhabdi	1261	73	6.1	322	2	Q9H6T9	HUMAN	Q9h6t9	homo sapien
1189	73.5	6.2	846	2	Q93U53	CARRU	Q93u53	carsonella	1262	73	6.1	326	2	Q99NR7	MUSAV	Q99nr7	muscardinus
1190	73.5	6.2	859	2	Q4YQV1	PLABE	Q4yqv1	plasmodium	1263	73	6.1	335	2	Q8SWL8	ENCUC	Q8swl8	encephalito
1191	73.5	6.2	881	2	Q5ZM00	CHICK	Q5zm00	gallus gall	1264	73	6.1	339	1	SRG7	CAEEL	P54129	caenorhabdi
1192	73.5	6.2	992	2	Q51315	ENTHI	Q51315	entamoeba h	1265	73	6.1	340	2	Q9N2T2	CAEEL	Q9n2t2	caenorhabdi
1193	73.5	6.2	1006	2	Q4YH96	PLABE	Q4yh96	plasmodium	1266	73	6.1	343	2	Q7YFU0	9HYME	Q7yfu0	myrmica sul
1194	73.5	6.2	1019	2	Q2KG26	MAGGR	Q2kg26	magnaporthe	1267	73	6.1	343	2	Q85AS7	UMASC	Q85as7	uma scopari
1195	73.5	6.2	1049	2	Q6FTY2	CANGA	Q6fty2	candida gla	1268	73	6.1	348	2	Q9TD49	9SMEG	Q9td49	cynolebias
1196	73.5	6.2	1095	2	Q9C7H5	ARATH	Q9c7h5	arabidopsis	1269	73	6.1	358	2	Q4E9M7	9RICK	Q4e9m7	wolbachia e
1197	73.5	6.2	1100	2	Q36ND8	MARHY	Q36nd8	marinobacte	1270	73	6.1	364	1	GHSR	MOUSE	Q99p50	mus musculu
1198	73.5	6.2	1174	2	Q7M006	9CORA	Q7m006	murine hepa	1271	73	6.1	364	1	GHSR	RAT	Q08725	rattus norv
1199	73.5	6.2	1175	2	Q4HDG2	CAMCO	Q4hdg2	campylobact	1272	73	6.1	375	2	Q86NC0	CAEEL	Q86nc0	caenorhabdi

1273	73	6.1	378	2	Q70EG4_9RODE	Q70EG4_saccostomus	1346	73	6.1	1127	2	Q9N323_CABEL	Q9n323 caenorhabdi
1274	73	6.1	378	2	Q70EG5_9RODE	Q70EG5_saccostomus	1347	73	6.1	1156	2	Q4WGM4_ASPPFU	Q4wgm4 aspergillus
1275	73	6.1	379	1	CYB_CRAFU	Q8WDV6_cratogeomys	1348	73	6.1	1268	2	Q553T5_DICDI	Q553t5 dictyosteli
1276	73	6.1	379	2	Q34099_CRAFU	Q34099_cratogeomys	1349	73	6.1	1931	2	Q8RJY3_STIAU	Q8rjy3 stigmatella
1277	73	6.1	379	2	Q698Q2_CRAFU	Q698q2_cratogeomys	1350	73	6.1	1951	2	Q7PZNT_ANOGA	Q7pzn7 anopheles g
1278	73	6.1	379	2	Q8WDV7_CRAFU	Q8WDV7_cratogeomys	1351	73	6.1	3010	2	P88803_9HEPC	P88803 hepatitis c
1279	73	6.1	383	2	Q9GL20_CYNBP	Q9GL20_cynopterus	1352	73	6.1	3010	2	Q9J3G1_9HEPC	Q9j3g1 hepatitis c
1280	73	6.1	391	1	Y450_BUCAP	Q8G999_buchnera ap	1353	73	6.1	3010	2	Q9J3I0_9HEPC	Q9j3i0 hepatitis c
1281	73	6.1	394	2	Q6EE99_LATCH	Q6EE99_lutimera c	1354	73	6.1	3013	2	Q9Q1A9_9HEPC	Q9q1a9 hepatitis c
1282	73	6.1	396	2	Q34FA7_9BURK	Q34FA7_burkholderi	1355	73	6.1	3013	2	Q9Q1Y0_9HEPC	Q9q1y0 hepatitis c
1283	73	6.1	396	2	Q44Y83_9BURK	Q44Y83_burkholderi	1356	73	6.1	6875	2	Q28733_RABIT	Q28733 cryptotlagus
1284	73	6.1	396	2	Q39KD3_BURS3	Q39kd3_burkholderi	1357	72.5	6.1	105	2	Q5ALK7_CANAL	Q5alk7 candida alb
1285	73	6.1	399	2	Q6LOJ3_PICTO	Q6loj3_picrophilus	1358	72.5	6.1	144	2	Q2LWL0_9DELT	Q2lwl0 syntrophus
1286	73	6.1	401	2	Q6KZX3_PICTO	Q6kzx3_picrophilus	1359	72.5	6.1	156	2	Q81516_9HEPC	Q81516 hepatitis c
1287	73	6.1	401	2	Q34D58_RHOPA	Q34d58_rhodospheudi	1360	72.5	6.1	156	2	Q81519_9HEPC	Q81519 hepatitis c
1288	73	6.1	412	2	Q61M38_CABER	Q61m38_caenorhabdi	1361	72.5	6.1	167	2	Q5KIU4_9RYNE	Q5kiu4 cryptococcus
1289	73	6.1	414	2	Q31S50_NATPD	Q31s50_natronomona	1362	72.5	6.1	170	2	Q2ULP6_ASPOR	Q2ulp6 aspergillus
1290	73	6.1	424	2	Q3AVM8_SYNS9	Q3avm8_synechococc	1363	72.5	6.1	173	2	Q9WD17_EAV	Q9wd17 equine arte
1291	73	6.1	437	2	Q4YN50_PLABE	Q4yn50_plasmodium	1364	72.5	6.1	174	2	P97065_9ENTR	P97065 salmonella
1292	73	6.1	446	2	Q8H9B3_BRACH	Q8h9b3_brassica ca	1365	72.5	6.1	180	2	P71252_ECOLI	P71252 escherichia
1293	73	6.1	450	1	VGLM_EHV1B	P28948_equine herp	1366	72.5	6.1	180	2	P71254_ECOLI	P71254 escherichia
1294	73	6.1	450	2	Q6SGV2_9ALPH	Q6sgv2_equid herpe	1367	72.5	6.1	180	2	P71255_ECOLI	P71255 escherichia
1295	73	6.1	452	2	Q36OL0_9GAMM	Q36ol0_shewanella	1368	72.5	6.1	180	2	P71256_ECOLI	P71256 escherichia
1296	73	6.1	453	2	Q43J07_CABEL	Q43j07_caenorhabdi	1369	72.5	6.1	180	2	P71258_ECOLI	P71258 escherichia
1297	73	6.1	461	2	Q4KJ6_STRPN	Q4kji6_streptococc	1370	72.5	6.1	180	2	P71259_ECOLI	P71259 escherichia
1298	73	6.1	461	2	Q9R923_STRPN	Q9r923_streptococc	1371	72.5	6.1	180	2	P71260_ECOLI	P71260 escherichia
1299	73	6.1	470	2	Q54PF0_DICDI	Q54pf0_dictyosteli	1372	72.5	6.1	180	2	P71261_ECOLI	P71261 escherichia
1300	73	6.1	474	2	Q94CI7_ARATH	Q94ci7_arabidopsis	1373	72.5	6.1	183	2	Q55TU2_CRYNE	Q55tj2 cryptococcus
1301	73	6.1	481	2	Q4K4Z1_PSEF5	Q4k4z1_pseudomonas	1374	72.5	6.1	191	2	Q8U4P0_PYRFU	Q8u4p0 pyrococcus
1302	73	6.1	487	2	Q37NN7_RHOPA	Q37nn7_rhodopseud	1375	72.5	6.1	208	2	O63447_ECHDI	O63447 echinotrix
1303	73	6.1	487	2	Q7MBA5_PHOLL	Q7mba5_photorhabdu	1376	72.5	6.1	208	2	Q7J7L2_ECHDI	Q7j7l2 echinotrix
1304	73	6.1	488	2	Q4HRT1_CAMUP	Q4hrt1_campylobact	1377	72.5	6.1	209	2	Q7J7L0_ECHDI	Q7j7l0 echinotrix
1305	73	6.1	494	1	KCNF1_HUMAN	Q9H3m0_homo sapien	1378	72.5	6.1	209	2	Q8GZ10_ARATH	Q8gz10 arabidopsis
1306	73	6.1	494	2	Q85L53_HUMAN	Q85l53_homo sapien	1379	72.5	6.1	209	2	Q49834_MYCLE	Q49834 mycobacteri
1307	73	6.1	509	2	Q5UCU7_CRYPV	Q5ucuk7_cryptospori	1380	72.5	6.1	210	2	Q7J7L9_ECHDI	Q7j7l9 echinotrix
1308	73	6.1	510	2	Q27072_TAESO	Q27072_tania soli	1381	72.5	6.1	211	2	Q7J7L3_ECHDI	Q7j7l3 echinotrix
1309	73	6.1	520	2	Q5KWR7_GEOKA	Q5kwr7_geobacillus	1382	72.5	6.1	214	2	O63950_ECHDI	O63950 echinotrix
1310	73	6.1	525	2	Q44WH7_CHLLI	Q44mh7_chlorobium	1383	72.5	6.1	217	2	Q9XMK7_OCHPR	Q9xmk7 ochotona pr
1311	73	6.1	546	2	Q5EAY8_XENLA	Q5eay8_xenopus lae	1384	72.5	6.1	220	2	Q40J90_EHRCH	Q40j90 ehrlichia c
1312	73	6.1	553	2	Q3MP12_CANAL	Q3mp12_candida alb	1385	72.5	6.1	222	2	Q31Y09_SHIBS	Q31y09 shigella bo
1313	73	6.1	553	2	Q99PN9_CANAL	Q99pn9_candida alb	1386	72.5	6.1	222	2	Q3YZU8_SHISS	Q3yzu8 shigella so
1314	73	6.1	553	2	Q9ZJU5_HELPJ	Q9zji5_helicobacte	1387	72.5	6.1	224	2	Q8RGE6_FUSNN	Q8rge6 fusobacteri
1315	73	6.1	556	2	Q7QZJ9_GIALA	Q7qzj9_giardia lam	1388	72.5	6.1	243	2	O4MHS9_BACCE	O4mhs9 bacillus ce
1316	73	6.1	597	2	Q2SRQ8_MYCCA	Q2srq8_mycoplasma	1389	72.5	6.1	255	2	Q7M2C0_LEIAM	Q7m2c0 leishmania
1317	73	6.1	599	2	Q3YOF7_ENTFC	Q3yof7_enterococcu	1390	72.5	6.1	267	2	Q3HA88_TRIER	Q3ha88 trichodesmi
1318	73	6.1	604	2	Q3V5J8_CABEL	Q3v5j8_caenorhabdi	1391	72.5	6.1	267	2	Q4S673_TETNG	Q4s673 tetraodon n
1319	73	6.1	616	2	Q6BIQ1_DEBHA	Q6biq1_debaryomyce	1392	72.5	6.1	269	2	Q8RES9_FUSNN	Q8res9 fusobacteri
1320	73	6.1	623	2	Q4RMH4_TETNG	Q4rmh4_tetradon n	1393	72.5	6.1	285	2	Q86DD6_CABEL	Q86dd6 caenorhabdi
1321	73	6.1	635	2	Q86X77_HUMAN	Q86x77_homo sapien	1394	72.5	6.1	288	2	O2WLM6_CLOBE	O2wlm6 clostridium
1322	73	6.1	643	2	Q7NBK6_MYCGA	Q7nbk6_mycoplasma	1395	72.5	6.1	291	2	O34561_MAIZE	O34561 zea mays (m
1323	73	6.1	668	2	Q9ALX8_BURPS	Q9alx8_burkholderi	1396	72.5	6.1	298	2	Q3WL74_BACSK	Q3wl74 bacillus cl
1324	73	6.1	668	2	Q63L61_BURPS	Q63l61_burkholderi	1397	72.5	6.1	298	2	Q8R2A8_MOUSE	Q8r2a8 mus musculu
1325	73	6.1	676	2	Q9VF31_DROME	Q9vf31_drosophila	1398	72.5	6.1	307	2	Q612V8_CABER	Q612v8 caenorhabdi
1326	73	6.1	676	2	Q2WL35_CLOBE	Q2wl35_clostridium	1399	72.5	6.1	308	2	Q6N472_RHOPA	Q6n472 rhodopseud
1327	73	6.1	703	2	Q4W5R5_CABEL	Q4w5r5_caenorhabdi	1400	72.5	6.1	309	2	Q71UE1_BOVIN	Q71ue1 bos taurus
1328	73	6.1	716	2	Q59LX3_CANAL	Q59lx3_candida alb	1401	72.5	6.1	310	2	Q5J2F7_CHIHI	Q5j2f7 chimarrogal
1329	73	6.1	788	1	FTSK_STAAM	P64164_staphylococ	1402	72.5	6.1	310	2	Q5WL95_BACSK	Q5wl95 bacillus cl
1330	73	6.1	788	1	FTSK_STAAC	P64165_staphylococ	1403	72.5	6.1	315	2	Q5WPB4_9DIPF	Q5wpb4 dermatobia
1331	73	6.1	789	1	FTSK_STAAC	Q5hgf5_staphylococ	1404	72.5	6.1	315	2	Q9LG02_ARATH	Q9lg02 arabidopsis
1332	73	6.1	789	1	FTSK_STAAR	Q6ghf9_staphylococ	1405	72.5	6.1	320	1	OXAAX2_LACLA	O9chz9 lactococcus
1333	73	6.1	806	2	Q5Z6J8_ORYSA	Q5z6j8_oryza sativ	1406	72.5	6.1	325	2	O9CII9_LACLA	O9cii9 lactococcus
1334	73	6.1	832	2	Q7UQF9_RHOBA	Q7udf9_rhodopirell	1407	72.5	6.1	336	2	O17077_CABEL	O17077 caenorhabdi
1335	73	6.1	844	2	Q6KYT8_PICTO	Q6kyt8_picrophilus	1408	72.5	6.1	348	2	Q833B9_ENTFA	Q833b9 enterococcu
1336	73	6.1	861	2	Q4DILA_TRYCR	Q4dil4_trypanosoma	1409	72.5	6.1	348	2	O99924_CYPINELA	O99924 cyprinella
1337	73	6.1	861	2	Q9AVX8_GUITH	Q9avx8_guillardia	1410	72.5	6.1	350	2	Q835L2_ENTFA	Q835l2 enterococcu
1338	73	6.1	966	1	PKD2_MOUSE	Q95245_mus musculu	1411	72.5	6.1	355	2	Q5UES6_ECOLI	Q5ues6 escherichia
1339	73	6.1	966	2	Q7TSI7_MOUSE	Q7tsi7_mus musculu	1412	72.5	6.1	356	2	O57A42_BRUAB	O57a42 bruceella ab
1340	73	6.1	966	2	Q8BPR6_MOUSE	Q8bpr6_mus musculu	1413	72.5	6.1	356	2	O8FXM4_BRUSA	O8fxm4 bruceella su
1341	73	6.1	971	2	O60337_HUMAN	Q60337_homo sapien	1414	72.5	6.1	356	2	Q2TIF9_BRUA2	Q2tif9 bruceella ab
1342	73	6.1	1035	2	Q967W1_SCHMA	Q967w1_schistosoma	1415	72.5	6.1	360	2	Q70US3_DRIRI	Q70us3 dirofiliaria
1343	73	6.1	1052	2	Q41D65_9BACI	Q41d65_exiguobacte	1416	72.5	6.1	363	2	Q6HGU9_BACHK	Q6hgu9 bacillus th
1344	73	6.1	1075	2	Q9LPE2_ARATH	Q9lpe2_arabidopsis	1417	72.5	6.1	365	2	Q41629_STAHI	Q41629 staphylococ
1345	73	6.1	1111	2	Q86FP2_CABEL	Q86fp2_caenorhabdi	1418	72.5	6.1	374	2	Q8WMR0_SHEEP	Q8wmr0 ovine aries

1419	Q4R215	VARHI	377	2	Q4R215	vargula hil	1492	72.5	6.1	567	2	Q4YT29	PLABE	Q4yt29 plasmodium	
1420	Q85av3	chimarrogal	379	1	Q85av3	chimarrogal	1493	72.5	6.1	574	2	Q2XIN5	9GAMM	Q2xln5 shewanella	
1421	Q9gb1y	ochotona al	379	1	Q9gb1y	ochotona al	1494	72.5	6.1	574	2	Q35VD8	9GAMM	Q35vd8 shewanella	
1422	Q9blb9	ochotona cu	379	1	Q9blb9	ochotona cu	1495	72.5	6.1	574	2	O6LH28	PHOPR	O6lh28 photobacter	
1423	Q9bgy6	ochotona hi	379	1	Q9bgy6	ochotona hi	1496	72.5	6.1	580	2	Q3X6Y0	METFL	Q3x6y0 methylobaci	
1424	Q9g6g2	ochotona hy	379	1	Q9g6g2	ochotona hy	1497	72.5	6.1	614	2	Q34X67	9GAMM	Q34x67 alkalilimni	
1425	Q9gbz0	ochotona ko	379	1	Q9gbz0	ochotona ko	1498	72.5	6.1	614	2	Q7U5J3	SYNPK	Q7u5j3 synecococc	
1426	Q9gbz1	ochotona la	379	1	Q9gbz1	ochotona la	1499	72.5	6.1	622	2	Q4B546	9BURK	Q4b546 polaromonas	
1427	Q9gbz2	ochotona nu	379	1	Q9gbz2	ochotona nu	1500	72.5	6.1	635	2	Q21335	CAEEL	Q21335 caenorhabdi	
1428	Q9gbz5	ochotona ro	379	1	Q9gbz5	ochotona ro									
1429	Q9bzul	ochotona ru	379	1	Q9bzul	ochotona ru									
1430	Q9gbz6	ochotona th	379	1	Q9gbz6	ochotona th									
1431	Q9gbz7	ochotona th	379	1	Q9gbz7	ochotona th									
1432	Q3lhy6	chimarrogal	379	2	Q3lhy6	chimarrogal									
1433	Q3lhy7	chimarrogal	379	2	Q3lhy7	chimarrogal									
1434	Q3lh20	CHIPT	379	2	Q3lh20	CHIPT									
1435	Q3lh22	CHIPT	379	2	Q3lh22	CHIPT									
1436	Q3lh27	CHIPT	379	2	Q3lh27	CHIPT									
1437	Q3LI03	CHIPT	379	2	Q3LI03	CHIPT									
1438	Q3LI07	CHIPT	379	2	Q3LI07	CHIPT									
1439	Q3LI15	CHIPT	379	2	Q3LI15	CHIPT									
1440	Q3LI18	CHIPT	379	2	Q3LI18	CHIPT									
1441	Q3LI21	CHIPT	379	2	Q3LI21	CHIPT									
1442	Q3LI32	CHIPT	379	2	Q3LI32	CHIPT									
1443	Q3LI39	CHIPT	379	2	Q3LI39	CHIPT									
1444	Q3LI49	CHIPT	379	2	Q3LI49	CHIPT									
1445	Q70UT5	OCHPR	379	2	Q70UT5	OCHPR									
1446	Q7ILX8	9LAGO	379	2	Q7ILX8	9LAGO									
1447	Q9G1C3	9LAGO	379	2	Q9G1C3	9LAGO									
1448	Q9G1C4	9LAGO	379	2	Q9G1C4	9LAGO									
1449	Q9GBY2	9LAGO	379	2	Q9GBY2	9LAGO									
1450	Q9GBY8	9LAGO	379	2	Q9GBY8	9LAGO									
1451	Q9GBY9	OCHHY	379	2	Q9GBY9	OCHHY									
1452	Q9GBZ3	OCHPA	379	2	Q9GBZ3	OCHPA									
1453	Q8EW16	MYCPE	379	2	Q8EW16	MYCPE									
1454	Q508J4	9RODE	379	2	Q508J4	9RODE									
1455	Q508J6	PERPA	379	2	Q508J6	PERPA									
1456	Q508P1	MICMC	379	2	Q508P1	MICMC									
1457	Q508P2	9RODE	379	2	Q508P2	9RODE									
1458	Q9GAW7	9RODE	379	2	Q9GAW7	9RODE									
1459	Q6RKp6	EBVG	387	2	Q6RKp6	EBVG									
1460	Q2MDP6	CROCR	388	2	Q2MDP6	CROCR									
1461	Q3XRY8	HUMAN	389	1	Q3XRY8	HUMAN									
1462	Q23827	SHIDS	395	2	Q23827	SHIDS									
1463	Q8WMO9	SHEEP	402	2	Q8WMO9	SHEEP									
1464	Q2SCC2	9GAMM	404	2	Q2SCC2	9GAMM									
1465	Q66cf9	YERPS	428	2	Q66cf9	YERPS									
1466	Q8ZG86	YERPE	428	2	Q8ZG86	YERPE									
1467	Q31E26	THICR	435	2	Q31E26	THICR									
1468	Q6L0Y3	PICTO	442	2	Q6L0Y3	PICTO									
1469	Q6PHK5	BRARE	442	2	Q6PHK5	BRARE									
1470	Q6NYH8	BRARE	445	2	Q6NYH8	BRARE									
1471	Q9T9N6	9BILA	452	2	Q9T9N6	9BILA									
1472	Q6P822	XENTR	457	2	Q6P822	XENTR									
1473	Q970D2	SULTO	478	2	Q970D2	SULTO									
1474	Q4HEC1	CAMCO	488	2	Q4HEC1	CAMCO									
1475	Q4HLN0	CAMLA	488	2	Q4HLN0	CAMLA									
1476	Q6SWJ8	CMNV	491	2	Q6SWJ8	CMNV									
1477	Q6QRY6	9BETA	499	1	Q6QRY6	9BETA									
1478	Q4APU8	9CHLB	505	2	Q4APU8	9CHLB									
1479	Q6QRY6	9BETA	509	2	Q6QRY6	9BETA									
1480	PACR	BOVIN	513	1	PACR	BOVIN									
1481	Q2RIT1	MOOTH	521	2	Q2RIT1	MOOTH									
1482	Q4QLJ3	HAE18	521	2	Q4QLJ3	HAE18									
1483	Q23444	CAEEL	522	2	Q23444	CAEEL									
1484	Q6FDF6	ACIAD	526	2	Q6FDF6	ACIAD									
1485	Q40LF0	DESAC	528	2	Q40LF0	DESAC									
1486	Q4RQ12	TETNG	528	2	Q4RQ12	TETNG									
1487	Q5CU37	CRYPV	539	2	Q5CU37	CRYPV									
1488	Q7VSL1	BORPE	539	2	Q7VSL1	BORPE									
1489	Q7W446	BORPE	539	2	Q7W446	BORPE									
1490	Q7WPK3	BORBR	539	2	Q7WPK3	BORBR									
1491	Q5F1M1	MYTGA	562	2	Q5F1M1	MYTGA									

ALIGNMENTS

RESULT 1

MENTO HUMAN

ID MENTO HUMAN STANDARD; PRT; 234 AA.

AC Q95772; 72.5 6.1 567 2 Q4YT29 PLABE

DT 15-NOV-2002, integrated into UniProtKB/Swiss-Prot.

DT 01-MAY-1999, sequence version 1.

DT 07-FEB-2006, entry version 39.

DE M64 N-terminal domain homolog (STARD3 N-terminal-like protein).

GN Name-STARD3NL; Synonyms=MENTHO; ORFNames=UNQ855/PRO1864;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE, CHARACTERIZATION, TOPOLOGY, PHOSPHORYLATION, AND

RP ALTERNATIVE INITIATION.

RC TISSUE=Fetal brain;

RX MEDLINE=22384343; PubMed=12393907; DOI=10.1074/jbc.M208290200;

RA Alpy P., Wendling C., Rio M.-C., Tomasetto C.;

RL "MENTHO, a MLN44 homologue devoid of the START domain.,"

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandera R.L., Watanabe C., Wileand D., Woods K., Xie M.-H., Goddard A.D.,

RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z.,

RA Wood W.I., Godowski P.J., Gray A.M.;

RA "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

RT bioinformatics assessment.,"

RL Genome Res. 13:2265-2270(2003).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=2737999; PubMed=12853948; DOI=10.1038/nature01782;

RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,

RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,

RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,

RA Fewell G.A., Delehaanty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,

RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,

RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,

RA Ozeresky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,

RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,

RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,

RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Stromatt C.,

RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,

RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,

RA Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,

RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,

RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,

RA Gillett W., Zhou Y., James R., Phelps K., Iadonoto S., Bubb K.,

RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,

RA Baertsch R.A., Brent M.R., Keibler E., Flicke P., Bork P., Suyama M.,

Db 1 MNHLPEDMENTLTGSSSHASLRDIHNSINPQLMARIESYEGREKKGISDVRRTFCLFVT 60
 QY 61 FDLFLVTLWTIENLVNGGIENTLEKVMQDYDYSSYDFIDFLLAVERFKVLILAYAVCRL 120
 Db 61 FDLFLVTLWTIENLVNGGIENTLUKKEVAHYDYSSYDFIDFLLAVERFKVLILAYAVCRL 120
 QY 121 RHWAIALTAVTSAFLAKVILSKLFSQAGFGVLPPIISFILAWIETWFLDFKVLPOEA 180
 Db 121 RHWAIALTAVTSAFLAKVILSKLFSQAGFGVLPPIISFILAWIETWFLDFKVLPOEA 180
 QY 181 EENRLLIVQASRAALIPGLSDGQFYPSPSEAGS-EBAEKQSEKPLLEL 234
 Db 181 EENRLLIVQASRAALIPAGLSDGQFYPSPSEAGSEBAEKQSEKPLLEL 235

RESULT 3

MENTO MOUSE STANDARD; PRT; 235 AA.
 AC Q9DCI3; Q99J63; Q90356;
 DT 15-NOV-2002, integrated into UniProtKB/Swiss-Prot.
 DT 15-NOV-2002, sequence version 2.
 DT 07-FEB-2006, entry version 29.
 DE MLN64 N-terminal domain homolog (STARD3 N-terminal-like protein).
 GN Name=Stard3n1; Synonyms=Mentho;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).

RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Kidney;
 RC PubMed=16141072; DOI=10.1126/science.1112014;
 EX Carninci P., Katayama T., Katayama S., Gough J., Frich M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Guetlich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sheng Y.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiyara K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Watnick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itch M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami T., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayaishizaki Y.;
 RT "the transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Mammary gland;
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
 membrane protein (by similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9DCI3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9DCI3-2; Sequence=VSP_003909;
 CC Note=No experimental confirmation available;
 CC -1- SIMILARITY: Contains 1 MENTAL domain.
 CC -1- CAUTION: Ref.1 (BAB31166) sequence differs from that shown due to
 a frameshift in position 31.
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 DR EMBL; AK002760; BAB22337.1; -; mRNA.
 DR EMBL; AK018331; BAB31166.1; ALT FRAME; mRNA.
 DR EMBL; BC003334; AA03334.1; -; mRNA.
 DR Ensembl; ENSMUSG0000003062; Mus musculus.
 DR MGI; MGI:1923455; Stard3n1.
 KW Alternative splicing; Membrane; Transmembrane.
 FT CHAIN 1 235 MLN64 N-terminal domain homolog.
 FT TRANSMEM 1 53 /FTID=PRO_0000096420.
 FT TOPO_DOM 54 74 Cytoplasmic (Potential).
 FT TRANSMEM 75 97 Extracellular (Potential).
 FT TOPO_DOM 98 118 Potential.
 FT TRANSMEM 119 122 Cytoplasmic (Potential).
 FT TOPO_DOM 123 143 Potential.
 FT TRANSMEM 144 150 Extracellular (Potential).
 FT TOPO_DOM 151 171 Potential.
 FT TRANSMEM 172 235 Cytoplasmic (Potential).
 FT DOMAIN 48 218 MENTAL.
 FT VARSPPLIC 218 235 SEEAARFKQSEKPLLEL -> NNSAFRMGIQKSSQPSGG
 AAGTARFVKPSSCREGRLPMWLQ (in isoform 2).
 FT FTID=VSP_003909.
 FT CONFLICT 32 33 QL -> HS (in Ref. 1; BAB22337).
 FT CONFLICT 52 52 R -> G (in Ref. 2).
 SQ SEQUENCE 235 AA; 26811 MW; F251725390CB1503 CRC64;
 Query Match 94.9%; Score 1134.5; DB 1; Length 235;
 Best Local Similarity 94.9%; Pred. No. 1.2e-94;
 Matches 223; Conservative 5; Mismatches 6; Indels 1; Gaps 1;
 QY 1 MNHLPEDMENTLTGSSSHASLRDIHNSINPQLMARIESYEGREKKGISDVRRTFCLFVT 60
 Db 1 MNHLPEDMENTLTGSSSHASLRDIHNSINPQLMARIESYEGREKKGISDVRRTFCLFVT 60

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu N., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuura T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura K., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AK152116; BAE30960.1; -; mRNA.
 DR MGI; MGI:1923455; Stard3n1.
 SQ SEQUENCE 235 AA; 26811 MW; F251725390CB1503 CRC64;

 Query Match 94.9%; Score 1134.5; DB 2; Length 235;
 Best Local Similarity 94.9%; Pred. No. 1.2e-94;
 Matches 223; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

 Qy 1 MNHLPEDENALTCQSASHSLRNHISNPTQLMARIESYEGREKKGISDVRRTFCFLVFT 60
 Db 1 MNHLPHEMENTLTCQSASHSLRDIHSINPAQLMARIESYEGREKKGISDVRRTFCFLVFT 60
 Qy 61 FDLFVTLTMIELNVNGGIENTLEKEVMQDYSSYDFIDFLAVFRPKVLILAYAVCRL 120
 Db 61 FDLFVTLTMIELNVNGGIENTLEKEVHYDYSSYDFIDFLAVFRPKVLILGYAVCRL 120
 Qy 121 RHWWAIALTTAVTSAFLAKVILSKLPSQAGFVGLPIISFILAWIETWFLDFKVLPOEA 180
 Db 121 RHWWAIALTTAVTSAFLAKVILSKLPSQAGFVGLPIISFILAWIETWFLDFKVLPOEA 180
 Qy 181 EENRLLIVODASRAALIPGLSDGQFSPSEAGS-EAEKQSEKPLLEL 234
 Db 181 EENRLLIVODASRAALIPAGLSGQFSPSEAGSEAEKQSEKPLLEL 235

 RESULT 5
 Q3U852_MOUSE PRELIMINARY; PRT; 235 AA.
 AC Q3U852;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 5.
 DE Bone marrow macrophage cDNA, RIKEN full-length enriched library,
 DE clone:1830067H03 product:STARD3 N-terminal like, full insert sequence.
 GN Name=Stard3n1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.

RX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Huminteki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.P., Lazarevic D., Lipovich L., Liu J.,
 RA Lluni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottaqui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Sheng Y.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiu K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Tesdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group
 RA (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Clothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Ferte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690 (2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Inotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,

RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: AK152378; BAE31167.1; -; mRNA.
DR MGI: MGI:1923455; Stardn1.
SQ SEQUENCE 235 AA; 26777 MW; AD55148C9FCF73D8 CRC64;
Query Match 94.4%; Score 1128.5; DB 2; Length 235;
Best Local Similarity 94.5%; Pred. No. 4.1e-94;
Matches 222; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
QY 1 MNHLPEDMENALTGSSQSHASLRNIHSINPTQMARISEYEGREKKGISDVRTTCLFVT 60
DB 1 MNHLPEDMENALTGSSQSHASLRNIHSINPTQMARISEYEGREKKGISDVRTTCLFVT 60
QY 61 FDLFPVTLIIELNVNGGIENTLKEVMQYDYSYDFIFLAVFRFKVLILAYAVCR 120
DB 61 FDLFPVTLIIELNVNGGIENTLKEVMQYDYSYDFIFLAVFRFKVLILAYAVCR 120
QY 121 RHWAIALTAVTSAPFLAKVILSKLFSQAGFYVLPIISFILAWIETWFLDFKVLPOA 180
DB 121 RHWAIALTAVTSAPFLAKVILSKLFSQAGFYVLPIISFILAWIETWFLDFKVLPOA 180
QY 181 EENRLLIVODASERAALIPGLSDGQFYSPPESEBAGS-EEAEKQDSKPLLEL 234
DB 181 EENRLLIVODASERAALIPGLSDGQFYSPPESEBAGS-EEAEKQDSKPLLEL 235
RESULT 6
Q6DI38 BRARE PRELIMINARY; PRT; 227 AA.
AC Q6DI38;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DE 07-FEB-2006, entry version 13.
DE STARD3 N-terminal like.
GN Name=stardn1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;

RG NTH MOC Project;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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 CC
 DR EMBL; BC075752; AAH75752.1; -; mRNA.
 DR Ensembl; ENSDARG00000045421; Danio rerio.
 DR ZFIN; ZDB-GENE-040718-4; stard3n1.
 SQ SEQUENCE 227 AA; 25485 MW; 24C46AD8FF4985C6 CRC64;

Query Match 66.6%; Score 796; DB 2; Length 227;
 Best Local Similarity 68.3%; Pred. No. 6.7e-64;
 Matches 155; Conservative 31; Mismatches 39; Indels 2; Gaps 2;

QY 8 MENALTSQSASHSLRNHISINPTQMARTSYEGREKKGISDVRRFTCLFVTFDILLFVT 67
 DB 1 MDSQSSSVSRAMGLGNGINSTPISARVESYAGEKKGISDVRRFTCLFVTFDILLFVT 60
 QY 68 LLWIIELNVNGGIENTLEKEVMQDYSSYFDFIPLAVFRPKVLILAYAVCRRLRHWMAIA 127
 DB 61 LLWIIELNVNGGIQQLLEQVLYKDYHKSFPDIFLLAVFRPAALILAYAVCKLRHWMAIA 120
 QY 128 LTTAVTSAPFLAKVLSKLSQAGFYVLPPIISFILAWIETWFLDFKVLPOEAEENRLL 187
 DB 121 ITTAITGFLIVKVVSKLLSQAGFYVLPPIISFILAWIETWFLDFKVLPOEAGDEIRYL 180
 QY 188 IVQDASERAALI-PGGLSDGQFYSPPESEAGS-EEASEKODSEKPLL 232
 DB 181 SVQNRLEHEPLLPGLPGLSEGLFYSPPESEAGSDESDLDKDHLEKPIV 227

RESULT 7
 Q6DFR7_XENTR PRELIMINARY; PRT; 448 AA.
 AC Q6DFR7;
 DT 16-AUG-2004, integrated into UniProtKB/TREMBL.
 DT 16-AUG-2004, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE START domain containing 3.
 GN Name-stard3-prov;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus; Silurana.
 OX NCBI_TaxID=8364;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Schaefer C.F., Bhat N.K.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Butterfield A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Rodriguez A.C., Schmutz J., Schmutz J., Schmutz J., Schmutz J.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;

RA Klein S., Gerhard D.S.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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 CC
 DR EMBL; BC076666; AAH76666.1; -; mRNA.
 DR SMR; Q6DFR7; 232-443.
 DR Ensembl; ENSKETG00000015141; Xenopus tropicalis.
 DR GO; GO:0015485; F:cholesterol binding; IEA.
 DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
 DR GO; GO:0006894; P:steroid biosynthesis; IEA.
 DR InterPro; IPR000799; StAR.
 DR InterPro; IPR002913; START_lipid_bd.
 DR Pfam; PF01852; START; 1.
 DR PRINTS; PR00978; STARPPOTEIN.
 DR SMART; SM00234; START; 1.
 DR PROSITE; PSS0848; START; 1.
 SQ SEQUENCE 448 AA; 50927 MW; 2686D07C737D4204 CRC64;

Query Match 58.6%; Score 700.5; DB 2; Length 448;
 Best Local Similarity 61.1%; Pred. No. 7.3e-55;
 Matches 143; Conservative 29; Mismatches 49; Indels 13; Gaps 4;

QY 1 MNHLP----EDMENALTSQSASHSLRNHISINPTQMARTSYEGREKKGISDVRRFTFC 56
 DB 1 MTKLPGDFQDLSRLSPATIASINSSMSQNHVSPHSLPR-----EQRRVISDVRRFTFC 54
 QY 57 LFTVFDLLFVTLWIIELNVNGGIENTLEKEVMQDYSSYFDFIPLAVFRPKVLILAYA 116
 DB 55 LFTVFDLLFVTLWIIELNVNGGIENTLEKEVMQDYSSYFDFIPLAVFRPKVLILAYA 114
 QY 117 VCLRLHWAIATLTAVTSAPFLAKVLSKLSQAGFYVLPPIISFILAWIETWFLDFKVL 176
 DB 115 IVRLRWMAIATLTAVTSAPFLAKVLSKLSQAGFYVLPPIISFILAWIETWFLDFKVL 174
 QY 177 PQEAEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSEAEKODSEK 229
 DB 175 TQEAEEERWYMAVQAAGSHPHPLVNGALSDGQFYSPPESEAGSD--NEPDDDEE 226

RESULT 8
 Q6PF40_XENLA PRELIMINARY; PRT; 444 AA.
 ID Q6PF40_XENLA PRELIMINARY; PRT; 444 AA.
 AC Q6PF40;
 DT 05-JUL-2004, integrated into UniProtKB/TREMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 14.
 DE MGC68989 protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Schaefer C.F., Bhat N.K.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Rodriguez A.C., Schmutz J., Schmutz J., Schmutz J., Schmutz J.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;

RESULT 10
MLN64 HUMAN
ID MLN64_HUMAN STANDARD; PRT; 445 AA.
AC Q14849; Q96HM9;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 51.
DE MLN 64 protein (STAR-related lipid transfer protein 3) (STARD3) (START
DE domain-containing protein 3) (CAB1 protein).
GN Name=STARD3; Synonyms=CAB1, MLN64;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Mammary carcinoma;
RX MEDLINE=96039245; PubMed=7490069;
RA Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
RA Chenard M.-P., Lidreau R., Bassot P., Rio M.-C.;
RT "Identification of four novel human genes amplified and overexpressed
RT in breast carcinoma and localized to the q11-q21.3 region of
RT chromosome 17.";
RL Genomics 28:367-376(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Oesophageal carcinoma;
RX MEDLINE=97413641; PubMed=9270027;
RA Akiyama N., Sasaki H., Ishizuka T., Kishi T., Sakamoto H., Onda M.,
RA Hirai H., Yazaki Y., Sugimura T., Terada M.;
RT "Isolation of a candidate gene, CAB1, for cholesterol transport to
RT mitochondria from the c-ERBB-2 amplicon by a modified cDNA selection
RT method.";
RL Cancer Res. 57:3548-3553(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lung, Skin, and Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ÅNGSTRÖMS) OF 216-445.
RX MEDLINE=20264523; PubMed=10802740; DOI=10.1038/75192;
RA Teujishita Y., Hurley J.H.;
RT "Structure and lipid transport mechanism of a STAR-related domain.";
RL Nat. Struct. Biol. 7:408-414(2000).
RN [5]
RP TOPOLOGY.
RX MEDLINE=21264925; PubMed=11053434; DOI=10.1074/jbc.M006279200;
RA Alpy F., Stoeckel M.-E., Dierich A., Escola J.-M., Wendling C.,
RA Chenard M.-P., Vanier M.T., Gruenberg J., Tomasetto C., Rio M.-C.;
RT "The steroidogenic acute regulatory protein homolog MLN64, a late
RT endosomal cholesterol-binding protein.";

RL J. Biol. Chem. 276:4261-4269(2001).
CC -I- FUNCTION: Binds and transports cholesterol. Promotes
CC steroidogenesis in placenta and brain.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC membrane protein.
CC -I- SIMILARITY: Contains 1 MENTAL domain.
CC -I- SIMILARITY: Contains 1 START domain.
CC -I- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/MLN64ID202.html".
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
EMBL; X80198; CAA56489.1; -; mRNA.
EMBL; D38255; BAA22525.1; -; mRNA.
EMBL; BC008356; AAH08356.1; -; mRNA.
EMBL; BC008747; AAH08747.1; -; mRNA.
EMBL; BC025679; AAH25679.1; -; mRNA.
PIR; I38027; I38027.
PDB; 1EM2; X-ray; A=216-444.
DR Ensembl; ENSG00000131748; Homo sapiens.
DR H-InvDB; HIX0013780; -;
DR HGNC; HGNC:17579; STARD3.
DR MIM; 607048; Gene.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0008203; P:cholesterol metabolism; TAS.
DR GO; GO:0006629; P:lipid metabolism; TAS.
DR GO; GO:0006839; P:mitochondrial transport; TAS.
DR GO; GO:0008202; P:steroid metabolism; TAS.
DR InterPro; IPR000799; STAR.
DR InterPro; IPR002913; START_lipid_bd.
DR Pfam; PF01852; STARPROTEIN.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS00848; START; 1.
KW 3D-structure; Lipid transport; Lipid-binding; Membrane;
KW Steroidogenesis; Transmembrane; Transport.
FT CHAIN 1 445 MLN 64 protein.
FT /FTID=PRO 000220653.
FT TOPO_DOM 1 51 Cytoplasmic (Potential).
FT TRANSMEM 52 72 Potential.
FT TOPO_DOM 73 94 Extracellular (Potential).
FT TRANSMEM 95 115 Potential.
FT TOPO_DOM 116 120 Cytoplasmic (Potential).
FT TRANSMEM 121 141 Potential.
FT TOPO_DOM 142 148 Extracellular (Potential).
FT TRANSMEM 149 169 Potential.
FT TOPO_DOM 170 445 Cytoplasmic (Potential).
FT DOMAIN 46 217 MENTAL.
FT DOMAIN 230 443 START.
FT CONFLICT 117 117 Q -> R (in Ref. 3; AAH08356/AAH25679).
FT CONFLICT 216 216 G -> A (in Ref. 3; AAH25679).
FT HELIX 233 258
FT STRAND 260 264
FT TURN 266 267
FT STRAND 270 276
FT TURN 277 279
FT STRAND 280 291
FT HELIX 293 299
FT TURN 300 302
FT HELIX 304 307
FT TURN 308 310
FT TURN 312 313
FT STRAND 314 323
FT TURN 324 326
FT STRAND 327 334
FT STRAND 337 337
FT TURN 338 341
FT STRAND 342 342
FT STRAND 345 355
FT STRAND 357 366
FT TURN 370 371
FT STRAND 372 372

FT TURN 376 377
FT STRAND 378 380
FT STRAND 382 383
FT STRAND 385 392
FT STRAND 394 395
FT TURN 397 398
FT STRAND 400 406
FT STRAND 408 409
FT STRAND 412 414
FT HELIX 416 440
FT TURN 441 442
SQ SEQUENCE 445 AA; 50474 MW; 62BED5C3EDA0DDEF CRC64;

Query Match 55.6%; Score 664; DB 1; Length 445;
Best Local Similarity 56.2%; Pred. No. 1.5e-51;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

QY 1 MNHLP-----EDMENAL-----TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
DB 1 MSKLPRELTRDLERSLPAVASGLSSLSHSLPPPE-----KRAAISDV 49
QY 52 RRTFCFLVTFDILLFVLLMIILNNGGIENTLEKEVMQDYSSYDFIFLLAVFRKVL 111
DB 50 RRTFCFLVTFDILLFISLLMIILNNGGIENTLEKEVMQDYSSYDFIFLLAVFRKVL 109
QY 112 ILAYAVCLRHWAIALTTAVTSFAFLAKVILSKLFSQAGFYVLPPIISFILAWIETWFL 171
DB 110 LLGYAVLQLRHWMVIAVTTLVSSAFLIVKVLSELLSKGAFGLLPVFSVLAWIETWFL 169
QY 172 DFKVLPQAEERENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEKQDSEK 229
DB 170 DFKVLPQAEERENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEKQDSEK 229

RESULT 11
Q53Y53 HUMAN PRELIMINARY; PRT; 445 AA.
AC Q53Y53;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE START domain containing 3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kalinine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
RT vector."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; BT006964; AAP35610.1; -; mRNA.
DR SMR; Q53Y53; 230-443.
DR Ensembl; ENSG00000131748; Homo sapiens.
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR GO; GO:0006694; P:steroid biosynthesis; IEA.
DR InterPro; IPR000799; STAR.
DR InterPro; IPR002913; START_lipid_bd.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS00848; START; 1.
SQ SEQUENCE 445 AA; 50474 MW; 62BED5C3EDA0DDEF CRC64;

Query Match 55.6%; Score 664; DB 2; Length 445;
Best Local Similarity 56.2%; Pred. No. 1.5e-51;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

QY 1 MNHLP-----EDMENAL-----TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
DB 1 MSKLPRELTRDLERSLPAVASGLSSLSHSLPPPE-----KRAAISDV 49
QY 52 RRTFCFLVTFDILLFVLLMIILNNGGIENTLEKEVMQDYSSYDFIFLLAVFRKVL 111
DB 50 RRTFCFLVTFDILLFISLLMIILNNGGIENTLEKEVMQDYSSYDFIFLLAVFRKVL 109
QY 112 ILAYAVCLRHWAIALTTAVTSFAFLAKVILSKLFSQAGFYVLPPIISFILAWIETWFL 171
DB 110 LLGYAVLQLRHWMVIAVTTLVSSAFLIVKVLSELLSKGAFGLLPVFSVLAWIETWFL 169
QY 172 DFKVLPQAEERENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEKQDSEK 229
DB 170 DFKVLPQAEERENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEKQDSEK 229

RESULT 12
MLN64 MOUSE STANDARD; PRT; 446 AA.
AC Q61542;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 45.
DE MLN 64 protein (Star-related lipid transfer protein 3) (STARD3) (START
DE domain-containing protein 3) (ES 64 protein).
GN Name=Stard3; Synonyms=Es64, MLN64;
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=96039245; PubMed=7490069;
RA Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
RA Chenard M.-P., Lidereau R., Basset P., Rio M.-C.;
RT "Identification of four novel human genes amplified and overexpressed
RT in breast carcinoma and localized to the q11-q21.3 region of
RT chromosome 17."
RL Genomics 28:367-376(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Binds and transports cholesterol. Promotes
CC steroidogenesis in placenta and brain (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC membrane protein (By similarity).

CC --!- SIMILARITY: Contains 1 MENTAL domain.
 CC --!- SIMILARITY: Contains 1 START domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR ENBL; X82457; CAA57834.1; -; mRNA.
 DR ENBL; BC003313; AA03313.1; -; mRNA.
 DR HSP; Q14849; 1EM2.
 DR SWR; Q61542; 231-444.
 DR Ensembl; ENSMUSG00000018167; Mus musculus.
 DR MGI; MGI.1929618; Stard3.
 DR GO; GO:0016021; C: integral to membrane; TAS.
 DR GO; GO:0005770; C: late endosome; TAS.
 DR InterPro; IPR000799; STAR.
 DR InterPro; IPR002913; START_lipid_bd.
 DR Pfam; PF01852; START; 1.
 DR PRINTS; PR00978; STARPROTEIN.
 DR SMART; SM00234; START; 1.
 DR PROSITE; PS00848; START; 1.
 DR Lipid transport; Lipid-binding; Membrane; Steroidogenesis;
 KW Transmembrane; Transport.
 FT CHAIN 1 446
 FT
 FT TOPO_DOM 1 52
 FT TRANSMEM 53 73
 FT TOPO_DOM 74 95
 FT TRANSMEM 96 116
 FT TOPO_DOM 117 121
 FT TRANSMEM 122 142
 FT TOPO_DOM 143 149
 FT TRANSMEM 150 170
 FT TOPO_DOM 171 446
 FT DOMAIN 47 218
 FT DOMAIN 231 444
 FT SEQUENCE 446 AA; 50470 MW; DFF4359604F3B1E2 CRC64;
 Query Match 54.9%; Score 656.5; DB 1; Length 446;
 Best Local Similarity 57.8%; Pred. No. 7.3e-51;
 Matches 133; Conservative 33; Mismatches 47; Indels 17; Gaps 4;
 QY 7 DMENAL-----TGSQSSHASLRNIHSINPOLMARIESYGRKKIGSDVRRFTCLVPTF 61
 Db 11 DLERSLPALASLTSLSHSQSLSSHSHTPPPL-----EKRAISDVRRFTCLVPTF 60
 QY 62 DLLFVTLITLIIENVNGGIENTLEKEVMQDYVSSYEDIELLAVFRFKVLILAYAVCLR 121
 Db 61 DLLFISLLITLIIENVNGGIENTLEKEVMQDYVSSYEDIELLAVFRFKVLILAYAVCLR 120
 QY 122 HWMIAITLTAFTSAFLAKVILSKLFSQAGFVGLPITISFILAWIETWFLDFKVLPOEAE 181
 Db 121 HWMVIAITLTAFTSAFLAKVILSKLFSQAGFVGLPITISFILAWIETWFLDFKVLPOEAE 180
 QY 182 EENRLIVQDSRAALI-PPGLSDGQFYSPPESEAGSE-EAEKQDSEK 229
 Db 181 EERWYLAQAQAAVARGPLLFSGALSEGQFYSPPESEAGSE-EAEKQDSEK 230
 RESULT 13
 Q544C3 MOUSE PRELIMINARY; PRT; 446 AA.
 AC Q544C3;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DE 3 days neonate thymus cDNA, RIKEN full-length enriched library,
 DE clone: A63020B16 product: steroidogenic acute regulatory protein
 DE related, full insert sequence (NOD-derived Cd1c +ve dendritic cells
 DE cDNA, RIKEN full-length enriched library, clone: F630202P06
 DE product: START domain containing 3, full insert sequence).
 GN Names: Stard3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Thymus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Thymus;
 RX PubMed=16141072; DOI=10.1126/science.11112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 Ambesi-Impombato A., Apweiler R., Attaliya R.N., Bono H., Chalk A.M.,
 Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 Fletcher C.P., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 Petrovsky N., Piazza S., Reed J., Reid J.P., Ring B.Z., Ringwald M.,
 Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 Sperling S., Stupka E., Sugiyara K., Sultana R., Takenaka Y., Taki K.,
 Tammoja K., Tan S.B., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 Gammann S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 Iida J., Inamura K., Itoh T., Kato T., Kawaji H., Kawagashira N.,
 Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Thymus;
 RX PubMed=16141073; DOI=10.1126/science.11112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J, and NOD; TISSUE=Thymus;
 RX MEDLINE=12466851; PubMed=101038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikaishi I., Oatso N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 Blake J.A., Bradt D., Brusic V., Chothia K., Corbani L.E., Cousins S.,
 Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RG NIH MGC Project;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC085872; AAH5872.1; -; mRNA.
DR SMR; Q5U2T5; 231-444.
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR GO; GO:0006994; P:steroid biosynthesis; IEA.
DR InterPro; IPR000799; SCAR.
DR InterPro; IPR002913; START_lipid_bd.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS00848; START; 1.
DR Hypothetical protein.
SQ SEQUENCE 446 AA; 50386 MW; 19BF58B56F09722F CRC64;

Query Match 54.9%; Score 656.5; DB 2; Length 446;
Best Local Similarity 56.2%; Pred. No. 7.3e-51;
Matches 135; Conservative 32; Mismatches 52; Indels 21; Gaps 4;

Qy 1 MNHLPEDMEN-----ALTGSSQSHASLRNTHSINPTQMARISEYEGREKKGISDV 51
Db 1 MSKLPGDLAGLERSLPALASLGLTSLGSSQSLSHFTIPPPLEKRV-----VSDV 50

Qy 52 RTFCLFVTEDLLFTVTLWIILNNGGIENTLEKEVMQDYSSYDFIPLAVFRKVL 111
Db 51 RTFCLFVTEDLLFISLLIETNTGIRKNLEQVHYHSFQSSPFDIFVLAFFRFSGL 110

Qy 112 ILAVACRLRHWWAIALTTAVTS AFLAKVILSKLFSQAGFYVLPISFIAMTWFL 171
Db 111 LLGAVLRLQHWVIAITLVSSAFLVVKVILSKLKGAFYVLPVLSFVLALETWFL 170

Qy 172 DFKVLPQAEENRLLIVQDASRAALI-PGGLSDGQFYSPPESEAGE-EAEKQDSEK 229
Db 171 DFKVLPQAEERVLAQAARVARGPLLFSGALSEGQFYSPPESEAGSDSESDVAGKK 230

RESULT 15
MLN64 BRARE
ID MLN64 BRARE STANDARD; PRT; 448 AA.
AC Q9DFS4; Q6PH03;

DT 06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-2005, sequence version 2.
DT 07-FEB-2006, entry version 21.
DE MLN64-like protein (START domain-containing protein 3).
GN Name-stard3; Synonyms=mln64;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=AB;
RG NIH - Zebrafish Gene Collection (ZGC) project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 210-448.
RX PubMed=11064158; DOI=10.1016/S0303-7207(00)00316-6;
RA Bauer M.P., Bridgman J.T., Langenau D.M., Johnson A.L., Goetz F.W.;
RT "Conservation of steroidogenic acute regulatory (STAR) protein
structure and expression in vertebrates";
RL Mol. Cell. Endocrinol. 168:119-125(2000).
CC -!- FUNCTION: Binds and transports cholesterol. Promotes
steroidogenesis (By similarity).
CC -!- SIMILARITY: Contains 1 START domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC056766; AAH56766.1; -; mRNA.
DR EMBL; AF258786; AAG28603.1; -; mRNA.
DR HSPB; Q14849; LEM2.
DR SMR; Q9DFS4; 232-443.
DR Ensembl; ENSDARG0000017809; Danio rerio.
DR ZFIN; ZDB-GENE-001120-2; stard3.
DR InterPro; IPR000799; STAR.
DR InterPro; IPR002913; START_lipid_bd.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS00848; START; 1.
DR Lipid transport; Lipid-binding; Steroidogenesis; Transport.
KW Lipid transport; Lipid-binding; Steroidogenesis; Transport.
FT CHAIN 1 448
FT DOMAIN 1 232 445
FT CONFLICT 216 220 YSPPEISAGSE -> PGRPRVRPRV (in Ref. 2).
FT SEQUENCE 448 AA; 50751 MW; 716A18C127B59C5D CRC64;

Query Match 52.9%; Score 632; DB 1; Length 448;
Best Local Similarity 70.9%; Pred. No. 1.2e-48;
Matches 127; Conservative 18; Mismatches 32; Indels 2; Gaps 2;

Qy 44 EKIGISDVRTFCLFVTEDLLFTVTLWIILNNGGIENTLEKEVMQDYSSYDFIPL 103
Db 43 ERKAFSDVRTFCLFVTEDLLFTVTLWIILNNGGIENTLEKEVMQDYSSYDFIPL 102

Qy 104 AVREFKVLILAVACRLRHWWAIALTTAVTS AFLAKVILSKLFSQAGFYVLPISFIL 163
Db 103 AVREFKVLILAVACRLRHWWAIALTTAVTS AFLAKVILSKLFSQAGFYVLPISFIL 162

Qy 164 AWIETWFLDFKVLFPQAEENRLLIVQDASRAALI-PGGLSDGQFYSPPESEAGE 220
Db 163 AWIETWFLDFKVLFPQAEENRLLIVQDASRAALI-PGGLSDGQFYSPPESEAGE 221

Search completed: December 30, 2006, 16:55:40
Job time : 366 secs

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